

FIG. 1A

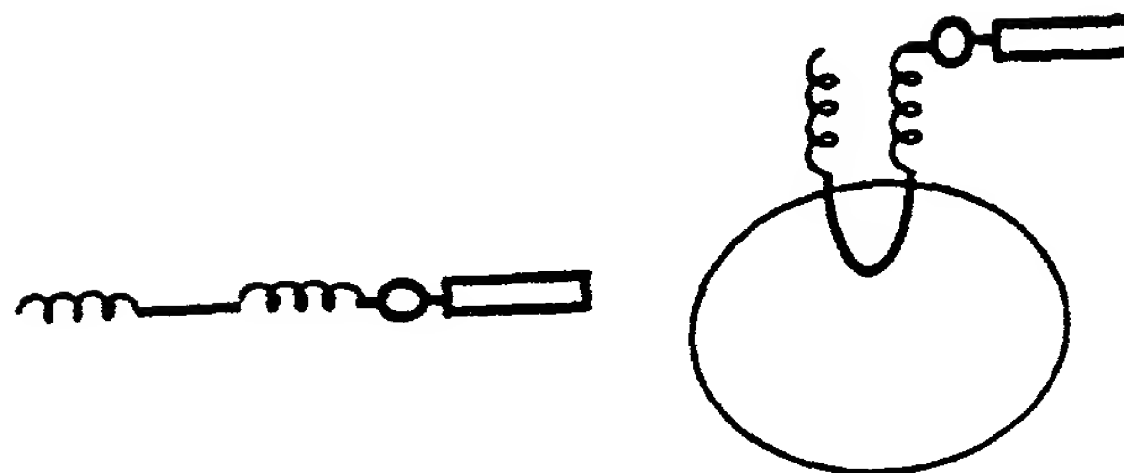


FIG. 1B

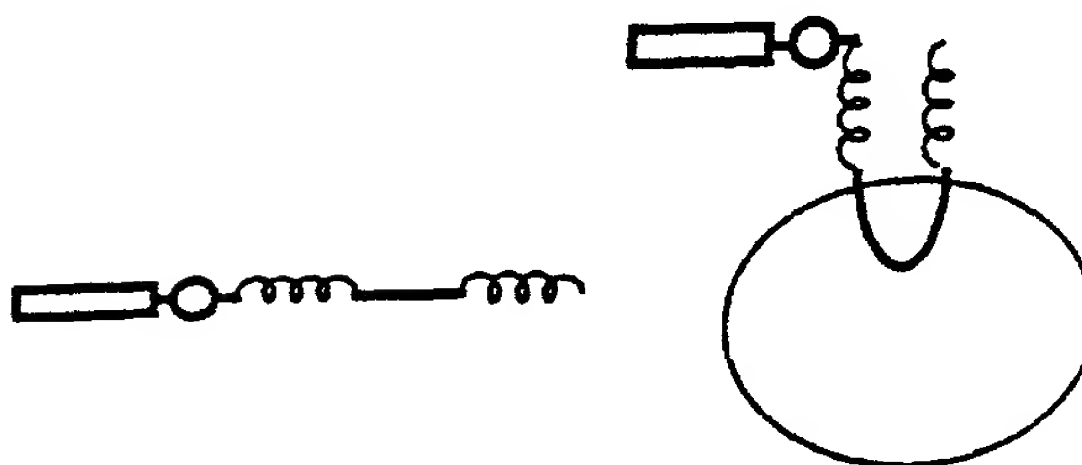


FIG. 1C

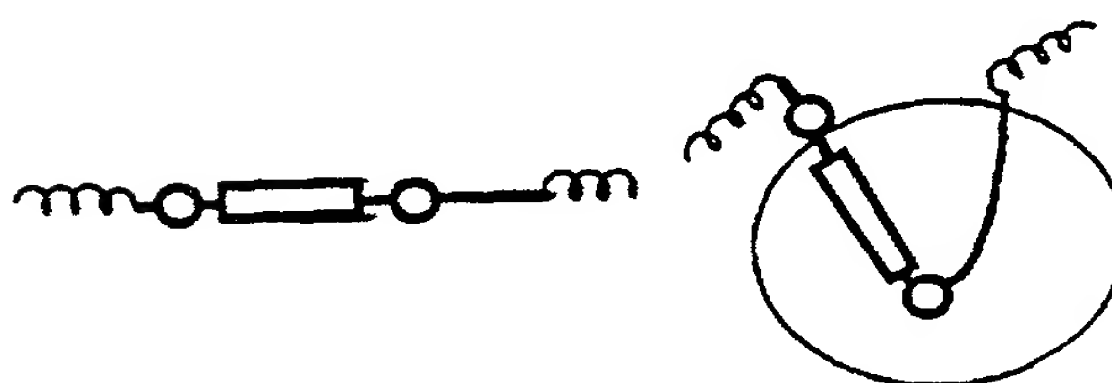


FIG. 1D

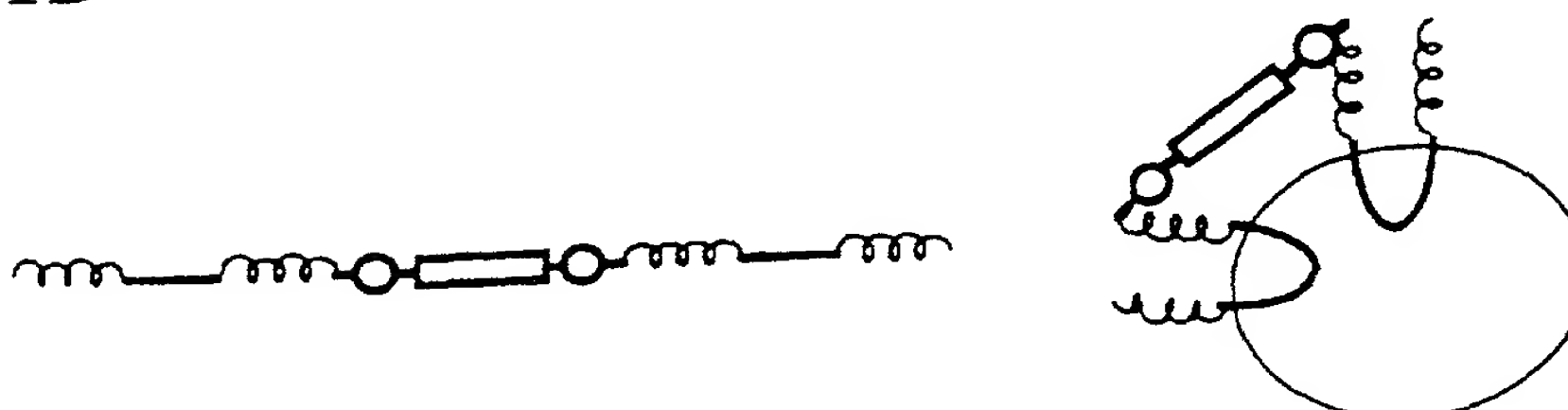


FIGURE 2

867 Not CCATGGCTATACCCAACCTCGGTCTTGGTCACACCAGGAACCTCTCTGGTAAGCTAGCTCCACTCCCCAGAAACAACCGGCGCCAAATTGC
777 CGGAATTGCTGACCTGAAGACGGAACATCATCGTCCGGTCTTGGGCGATTGCGGCGGAAGATGGGTGAGCTTGGGCTTGAGGACGAGAC
687 CGGAATCGAGTCTGTGAAAGGTTGTTTATTGGGATTGTTATACCGAGATTGGTCTGAGAGGTTTGAGGGAAAGGACAAATGGGTTTG
R1
597 GCTCTGGAGAAAGAGAGTGGGCTTTAGAGAGAGAAATTGAGAGCTTTAGAGAGAGATGCGGCGGCGATGACGGGAGGAGAGACGACGAGG
R2 R2
507 ACCTGCATTATCAAAGCAGTGACGTGGTGAAATTTGGAACCTTTTATGAGGCAGATAGATTTATTATTGTTATCCATTTTCTTTCATTGTTT
R1
417 TAGAATGTCCGGAACAAATTTTAAACTAAATCCTAAATTTTCTAATTTTGTGCAATAGTGGATATGTGGGCCGTATAGAAGGAAT
327 CTATTGAAGGCCAAACCCATCTGACGAGCCCAAGGTTTCGTTTTCGTTTATGTTTTCGTTTCGATGCCAACGCCACATTCTGAGCTA
I
237 GGCAAAAACAAACGTGTCTTTGAATAGACTCCTCTCGTTTAAACATGACAGGGCTGCATGGTGACGCCATTAAACAGTGGCCCTACAATT
147 GCATGATGTCTCCATTGACACGTGACTTCTCGTCTCCTTTCTTAATATATCTAACAAACACTCCTACCTCTTCCAAAATATATACACATC
57 TTTTGTGCAATCTCTCATTCAAAATCTCATTCTCTCTAGTAAACAAGAACAAAAAATGGCGGATACAGCTAGAGGAACCCATCAGAT
M A D T A R G T H H D
34 ATCATCGGCAGAGACCACTACCCGATGATGGGCGGAGACCGAGACCACTACAGATGTCCGGACGAGGATCTGACTACTCCAAGTCTAGG
I I G R D O Y P M M G R D R D O Y Q M S G R G S D Y S K S R
124 CAGATTGCTAAAGCTGCAACTGCTGTACAGCTGGTGGTTCCCTCCTTGTCTCTCCAGCCTTACCCTTGTGGAAGTGTATAGCTTTG
O I A K A A T A V T A G G S L L V L S S L T L V G T V I A L
214 ACTGTTGCAACACCTCTGCTGCTTATCTTCAGCCCAATCCTTGTCCCGGCTCTCATCAGTTGCACTCCTCATCACCGGTTTCTTTCC
T V A T P L L V I F S P I L V P A L I T V A L L I T G F L S
304 TCTGGAGGGTTTGGCATTTGCCGCTATAACCGTTTCTCTTGGATTTACAAgtaagcacacatttatcatcttacttcataattttgtgca
S G G F G I A A I T V F S W I Y K
394 atatgtgcatgcatgtgttgagccagtagctttggatcaatttttttggtcgaataacaaatgtaacaataagaaattgcaaatttctagg
484 gaacatttggttaactaaatacgaattttgacctagctagcttgaatgtgtctgtgtatatcatctatataggtaaaatgcttggtatga
Y A T G E H P Q G S D K L D S A R M K L G S K
574 tacctattgattgtgaatagGTACGCAACGGGAGAGACCCACAGGGATCAGACAAAGTTGGACAGTGCAAGGATGAAGTTGGGAAGCAAA
A O D L K D R A Q Y Y G Q Q H T G G E H D R D R T R G G Q H
664 GCTCAGGATCTGAAAGACAGAGCTCAGTACTACGACAGCAACATACTGGTGGGGAACATGACCGTGACCGTACTGTTGGTGGCCAGCAC
T T *
754 ACTACTTAAGTTACCCCACTGATGTCTCATAGTCCAATAACTCCAATGTTCGGGAGTTAGTTTATGAGGAATAAGTGTTTAGAAT
844 TTGATCAGGGGAGATATTAAGCCGAGTTTGAATCTTTTTGTTATAAGTAATGTTTATGTGTGTTTCTATATGTTGTCAAATGGTACC
KpnI

FIGURE 3

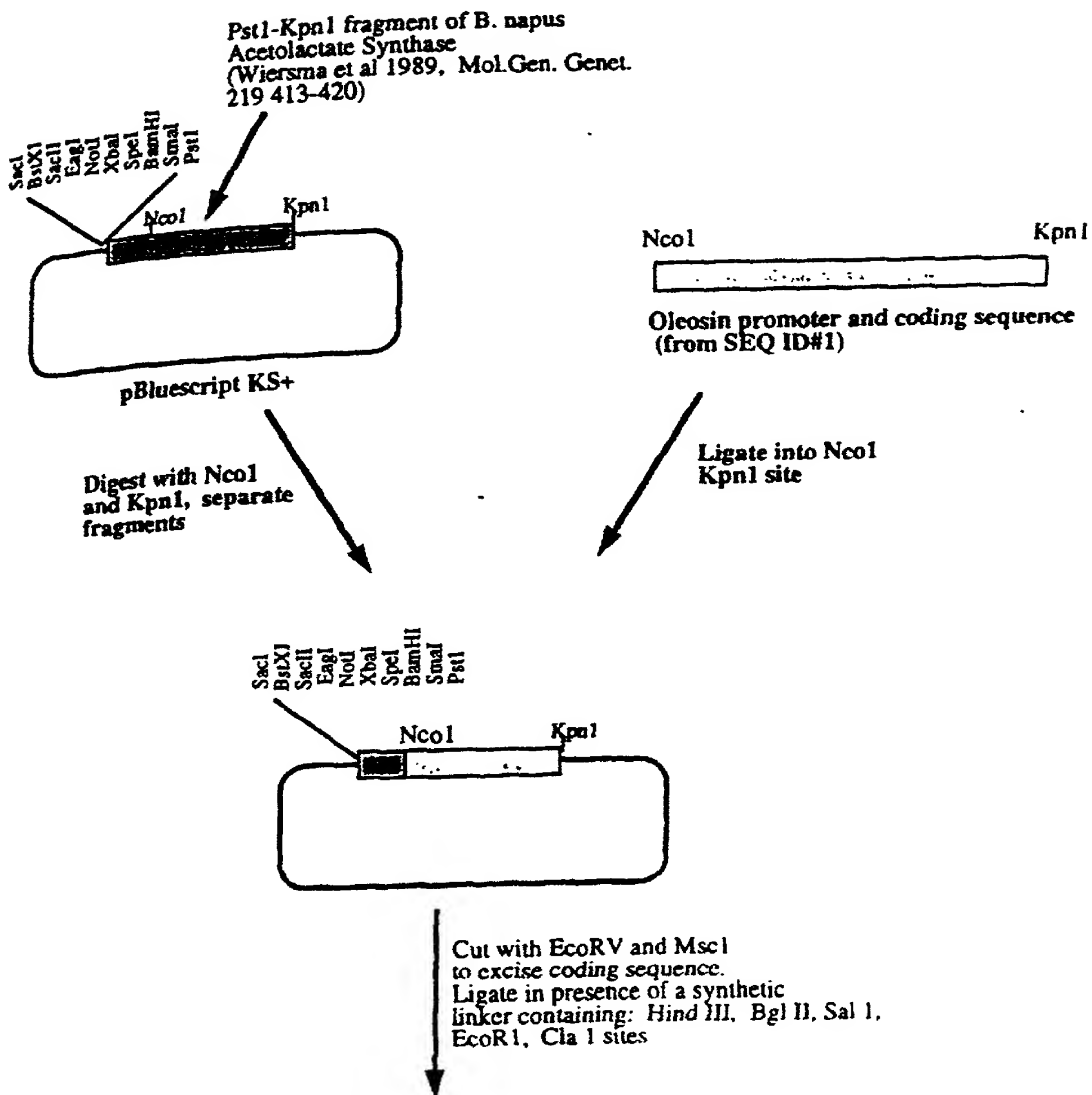


FIGURE 3 cont'd

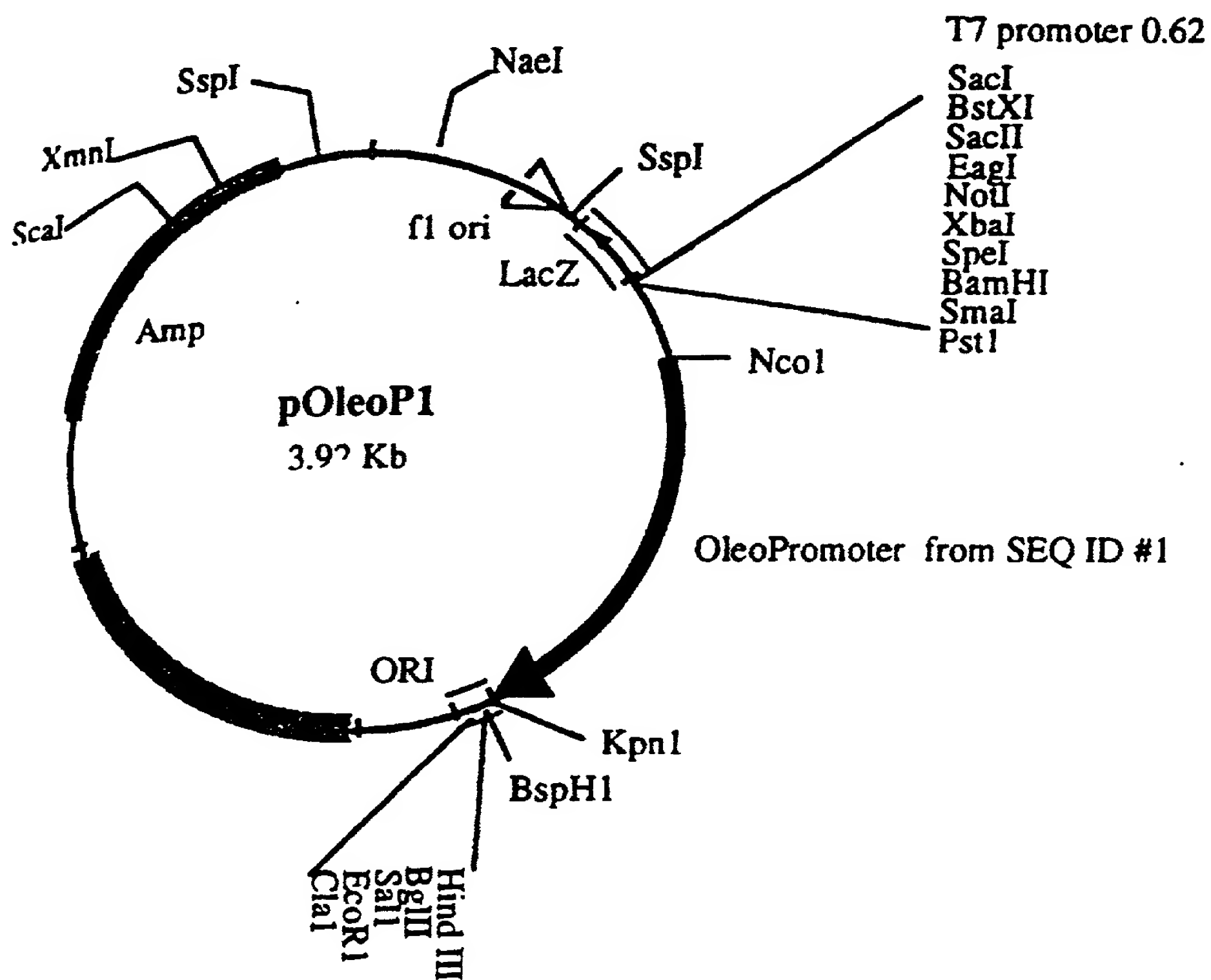


FIGURE 4

1 ATG GCG GAT ACA GCT AGA ACC CAT CAC GAT GTC ACA AGT CGA GAT CAG TAT CCC CGA GAC 60
1 M A D T A R T H H D V T S R D Q Y P R D 20

61 CGA GAC CAG TAT TCT ATG ATC GGT CGA GAC CGT GAC CAG TAC TCT ATG ATG GGC CGA GAC 120
21 R D Q Y S M I G R D R D Q Y S M M G R D 40

121 CGA GAC CAG TAC AAC ATG TAT GGT CGA GAC TAC TCC AAG TCT AGA CAG ATT GCT AAG GCT 180
41 R D Q Y N M Y G R D Y S K S R Q I A K A 60

181 GTT ACC GCA GTC ACG GCG GGT GGG TCC CTC CTT GTC CTC TCC AGT CTC ACC CTT GTT GGT 240
61 V T A V T A G G S L L V L S S L T L V G 80

241 ACT GTC ATT GCT TTG ACT GTT GCC ACT CCA CTC CTC GTT ATC TTT AGC CCA ATC CTC GTG 300
81 T V I A L T V A T P L L V I F S P I L V 100

301 CCG GCT CTC ATC ACC GTA GCA CTT CTC ATC ACT GGC TTT CTC TCC TCT GGT GGG TTT GCC 360
101 P A L I T V A L L I T G F L S S G G F A 120

361 ATT GCA GCT ATA ACC GTC TTC TCC TGG ATC TAT AAG TAC GCA ACG GGA GAG CAC CCA CAG 420
121 I A A I T V F S W I Y K Y A T G E H P Q 140

421 GCG TCA GAT AAG TTG GAC AGT GCA AGG ATG AAG CTG GGA ACC AAA GCT CAG GAT ATT AAA 480
141 G S D K L D S A R M K L G T K A Q D I K 160

481 GAC AGA GCT CAA TAC TAC GGA CAG CAA CAT ACA GGT GGT GAG CAT GAC CGT GAC CGT ACT 540
161 D R A Q Y Y G Q Q H T G G E H D R D R T 180

541 CGT GGT GGC CAG CAC ACT ACT TAA 564
181 R G G Q H T T *

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The diagram illustrates the construction of the pKKoleoGUS vector through a series of cloning steps:

- pGUSL318 (4853 bp):** Contains the GUS N358N>S gene, ORI, Ap^r, and a multiple cloning site (MCS) with restriction sites: SacI, BstXI, SacII, EcoI, NotI, XbaI, SpeI, BamHI, and NcoI.
- pKK233-2 (4593 bp):** Contains the P_{trc} promoter, SS (Shuttle Signal), Amp^r, and ori.
- Intermediate Vector (6486 bp):** Formed by inserting the GUS gene from pGUSL318 into pKK233-2. The MCS sites are EcoRI, EcoRV, HindIII, and PstI.
- pcDNA8 (3246 bp):** Contains the cDNA oleosin gene, ORI, Ap^r, and a multiple cloning site (MCS) with restriction sites: EcoRI, SacI, KpnI, NcoI, BamHI, BamHI, SalI, AccI, HincII, PstI, SphI, and HindIII.
- pKKoleoGUS (7046 bp):** The final construct, formed by inserting the cDNA oleosin fragment from pcDNA8 into the intermediate vector. The MCS sites are EcoRI, EcoRV, HindIII, and PstI.

FIGURE 6

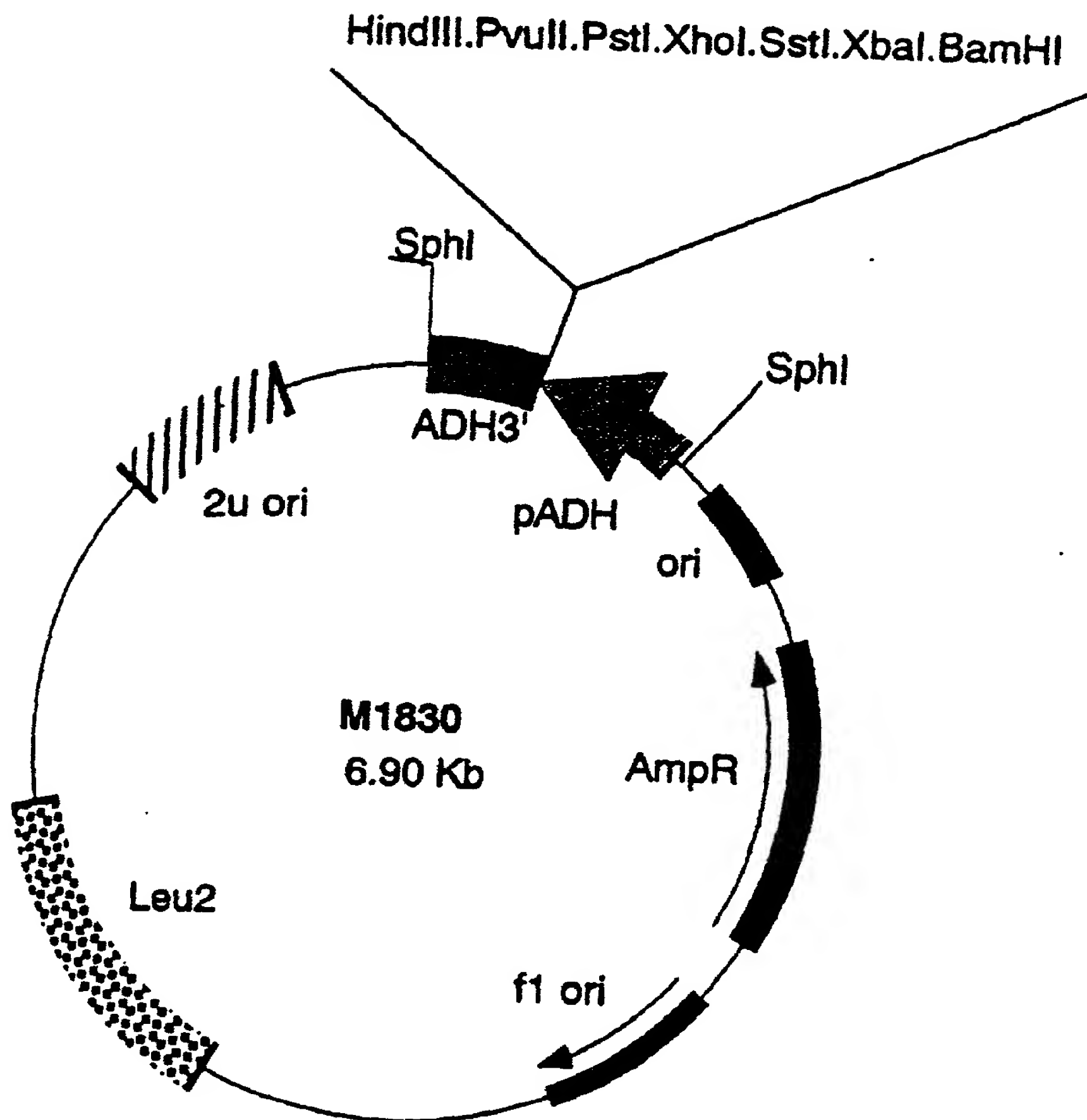
HindIII

1	ATAAGCTTGCATGCCTGCGGA	ACTCTCTGGTAAGCTAGCTCCACTCCCCAGAAACAACCG	60
61	CGCCAAATTGCCGGAATTGCTGACCTGAAGACGGAACATCATCGTCGGGTCTTGGGCG		120
121	ATTGCGGCGGAAGATGGGTCAGCTTGGGCTTGAGGACGAGACCCGAATCGAGTCTGTTGA		180
181	AAGGTTGTTTCATTGGGATTTGTATACGGAGATTGGTCGTCGAGAGGTTTGAGGGAAAGGA		240
241	CAAATGGGTTTGGCTCTGGAGAAAGAGAGTGC	GGGCTTTAGAGAGAGAATTGAGAGGTTTA	300
301	GAGAGAGATGCGGCGCGATGACGGGAGGAGAGACGACGAGGACCTGCATTATCAAAGCA		360
361	GTGACGTGGTGAAATTTGGA	ACTTTTAAGAGGCAGATAGATTTATTATTTGTATCCATTT	420
421	TCTTCATTGTTCTAGAATGTCGCGGAACAAATTTTAA	AACTAAATCCTAAATTTTCTAA	480
481	TTTGTGTTGCCAATAGTGGATATGTGGGCGGTATAGAAGGAATCTATTGAAGGCCCAAACC		540
541	CATACTGACGAGCCCAAAGGTTTCGTTTTGCGTTTTATGTTTCGGTTCGATGCCAACGCCA		600
601	CATTCTGAGCTAGGCAAAAAACAAACGTGTCTTTGAATAGACTCCTCTCGTTAACACATG		660
661	CAGCGGCTGCATGGTGACGCCATTAACACGTGGCCTACAATTGCATGATGTCTCCATTGA		720
721	CACGTGACTTCTCGTCTCCTTTCTTAATATATCTAACAAACACTCCTACCTCTTCCAAAA		780
781	TATATACACATCTTTTTGATCAATCTCTCATTCAA	AATCTCATTCTCTCTAGTAAACAAG	840
	M A D T A R G T H H D I I G R D Q		
841	AACAAAAAATGGCGGATACAGCTAGAGGAACCCATCAGGATATCATCGGCAGAGACCAG		900
	Y P M M G R D R D Q Y Q M S G R G S D Y		
901	TACCCGATGATGGGCGGAGACCGAGACCAGTACCAGATGTCCGGACGAGGATCTGACTAC		960
	S K S R Q I A K A A T A V T A G G S L L		
961	TCCAAGTCTAGGCAGATTGCTAAAGCTGCAACTGCTGTCACAGCTGGTGGTTCCTCCTT		1020
	V L S S L T L V G T V I A L T V A T P L		
1021	GTTCTCTCCAGCCTTACCCTTGTGGA	ACTGTCATAGCTTTGACTGTTGCAACACCTCTG	1080
	L V I F S P I L V P A L I T V A L L I T		
1081	CTCGTTATCTTCAGCCCAATCCTTGTCCCGGCTCTCATCACAGTTGCACTCCTCATCACC		1140
	G F L S S G G F G I A A I T V F S W I Y		
1141	GGTTTTCTTCTCTGAGGGTTTGGCATTGCCGCTATAACCGTTTTCTCTTGGATTAC		1200
	K		
1201	AAGTAAGCACACATTTATCATCTTACTTCATAATTTTGTGCAATATGTGCATGCATGTGT		1260
1261	TGAGCCAGTAGCTTTGGATCAATTTTTTTGGT	CGAATAACAAATGTAACAATAAGAAATT	1320
1321	GCAAATCTAGGGAACATTTGGTTAACTAAATACGAAATTTGACCTAGCTAGCTTGAATG		1380
1381	TGCTGTGTATATCATCTATATAGGTAAATGCTTGGTATGATACCTATTGATTGTGAAT		1440
	Y A T G E H P Q G S D K L D S A R M K		
1441	AGGTACGCAACGGGAGAGCACCCACAGGGATCAGACAAGTTGGACAGTGCAAGGATGAAG		1500
	L G S K A Q D L K D R A Q Y Y G Q Q H T		
1501	TTGGGAAGCAAAGCTCAGGATCTGAAAGACAGAGCTCAGTACTACGGACAGCAACATACT		1560
	G G E H D R D R T R G G Q H T T L V P R		
1561	GGTGGGGAACATGACCGTGACCGTACTCGTGGTGGCCAGCACACTACTCTCGTTCCACGA		1620
	G S M A E I T R I P L Y K G K S L R K A		
1621	GGATCCATGGCTGAGATCACCAGGATCCCTCTGTACAAAGGCAAGTCTCTGAGGAAGGCG		1680
	L K E H G L L E D F L Q K Q Q Y G I S S		
1681	CTGAAGGAGCATGGGCTTCTGGAGGACTTCCTGCAGAAACAGCAGTATGGCATCAGCAGC		1740
	K Y S G F G E V A S V P L T N Y L D S Q		
1741	AAGTACTCCGGCTTCGGGGAGGTGGCCAGCGTGCCCTGACCAACTACCTGGATAGTCAG		1800

FIGURE 6 cont'd

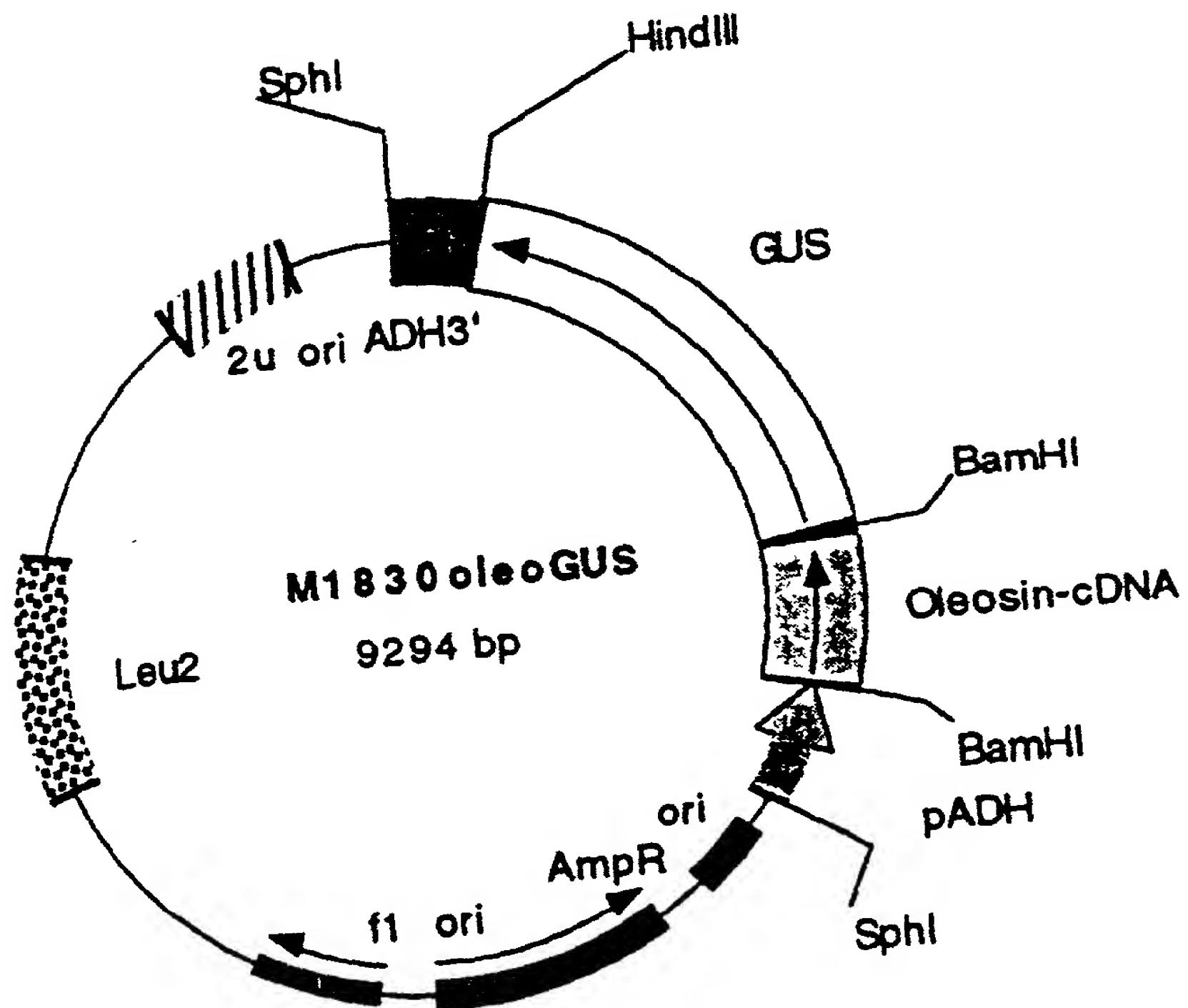
Y F G K I Y L G T P P Q E F T V L F D T
1801 TACTTTGGGAAGATCTACCTCGGGACCCCGCCCCAGGAGTTACCCGTGCTGTTTGACACT 1860
G S S D F W V P S I Y C K S N A C K N H
1861 GGCTCCTCTGACTTCTGGGTACCCTCTATCTACTGCAAGAGCAATGCCTGCAAAAACCAC 1920
Q R F D P R K S S T F Q N L G K P L S I
1921 CAGCGCTTCGACCCGAGAAAGTCGTCCACCTTCCAGAACCTGGGCAAGCCCCTGTCTATC 1980
H Y G T G S M Q G I L G Y D T V T V S N
1981 CACTACGGGACAGGCAGCATGCAGGGCATCCTGGGCTATGACACCGTCACTGTCTCCAAC 2040
I V D I Q Q T V G L S T Q E P G D V F T
2041 ATTGTGGACATCCAGCAGACAGTAGGCCTGAGCACCCAGGAGCCCGGGGACGTCTTCACC 2100
Y A E F D G I L G M A Y P S L A S E Y S
2101 TATGCCGAATTCGACGGGATCCTGGGGATGGCCTACCCCTCGCTCGCCTCAGAGTACTCG 2160
I P V F D N M M N R H L V A Q D L F S V
2161 ATACCCGTGTTTGACAACATGATGAACAGGCACCTGGTGGCCCAAGACCTGTTCTCGGTT 2220
Y M D R N G Q E S M L T L G A I D P S Y
2221 TACATGGACAGGAATGGCCAGGAGAGCATGCTCAGCTGGGGGCCATCGACCCGTCCTAC 2280
Y T G S L H W V P V T V Q Q Y W Q F T V
2281 TACACAGGGTCCCTGCACTGGGTGCCCCTGACAGTGCAGCAGTACTGGCAGTTCACTGTG 2340
D S V T I S G V V V A C E G G C Q A I L
2341 GACAGTGTCAACATCAGCGGTGTGGTTGTGGCCTGTGAGGGTGGCTGTCAGGCCATCTTG 2400
D T G T S K L V G P S S D I L N I Q Q A
2401 GACACGGGCACCTCCAAGCTGGTTCGGGCCCAGCAGCGACATCCTCAACATCCAGCAGGCC 2460
I G A T Q N Q Y G E F D I D C D N L S Y
2461 ATTGGAGCCACACAGAACCAGTACGGTGAGTTTGACATCGACTGCGACAACCTGAGCTAC 2520
M P T V V F E I N G K M Y P L T P S A Y
2521 ATGCCCACTGTGGTCTTTGAGATCAATGGCAAAATGTACCCACTGACCCCTCCGCCTAT 2580
T S Q D Q G F C T S G F Q S E N H S Q K
2581 ACCAGCCAAGACCAGGGCTTCTGTACCAGTGGCTTCCAGAGTGAAAATCATTCCCAGAAA 2640
W I L G D V F I R E Y Y S V F D R A N N
2641 TGGATCCTGGGGGATGTTTTTCATCCGAGAGTATTACAGCGTCTTTGACAGGGCCAACAAC 2700
L V G L A K A I *
2701 CTCGTGGGGCTGGCCAAAGCCATCTGAAAGCTT 2733
HindIII

FIGURE 7



034547-0106

FIGURE 8



ClustalW Formatted Alignments

10 20 30 40 50 60

TR
ATTHIREDB

70 80 90 100 110 120

TR
ATTHIREDB

130 140 150 160 170 180

TR
ATTHIREDB

190 200 210 220 230 240

TR
ATTHIREDB

250 260 270 280 290 300

TR
ATTHIREDB

310 320 330 340 350 360

TR
ATTHIREDB

370 380 390 400 410 420

TR
ATTHIREDB

430 440 450 460 470 480

TR
ATTHIREDB

490 500 510 520 530 540

TR
ATTHIREDB

550 560 570 580 590 600

TR
ATTHIREDB

610 620 630 640 650 660

TR
ATTHIREDB

670 680 690 700 710 720

TR
ATTHIREDB

730 740 750 760 770 780

TR
ATTHIREDB

790 800 810 820 830 840

TR
ATTHIREDB

850 860 870 880 890 900

TR
ATTHIREDB

910 920 930 940 950 960

TR
ATTHIREDB

970 980 990 1000 1010 1020

TR
ATTHIREDB

FIGURE 10

1	ATG	AAT	GGT	CTC	GAA	ACT	CAC	AAC	ACA	AGG	CTC	TGT	ATC	GTA	GGA	AGT	GGC	CCA	GCG	GCA	60
1	M	N	G	L	E	T	H	N	T	R	L	C	I	V	G	S	G	P	A	A	20
61	CAC	ACG	GCG	GCG	ATT	TAC	GCA	GCT	AGG	GCT	GAA	CTT	AAA	CCT	CTT	CTC	TTC	GAA	GGA	TGG	120
21	H	T	A	A	I	Y	A	A	R	A	E	L	K	P	L	L	F	E	G	W	40
121	ATG	GCT	AAC	GAC	ATC	GCT	CCC	GGT	GGT	CAA	CTA	ACA	ACC	ACC	ACC	GAC	GTC	GAG	AAT	TTC	180
41	M	A	N	D	I	A	P	G	G	Q	L	T	T	T	T	D	V	E	N	F	60
181	CCC	GGA	TTT	CCA	GAA	GGT	ATT	CTC	GGA	GTA	GAG	CTC	ACT	GAC	AAA	TTC	CGT	AAA	CAA	TCG	240
61	P	G	F	P	E	G	I	L	G	V	E	L	T	D	K	F	R	K	Q	S	80
241	GAG	CGA	TTC	GGT	ACT	ACG	ATA	TTT	ACA	GAG	ACG	GTG	ACG	AAA	GTC	GAT	TTC	TCT	TCG	AAA	300
81	E	R	F	G	T	T	I	F	T	E	T	V	T	K	V	D	F	S	S	K	100
301	CCG	TTT	AAG	CTA	TTC	ACA	GAT	TCA	AAA	GCC	ATT	CTC	GCT	GAC	GCT	GTG	ATT	CTC	GCT	ACT	360
101	P	F	K	L	F	T	D	S	K	A	I	L	A	D	A	V	I	L	A	T	120
361	GGA	GCT	GTG	GCT	AAG	CGG	CTT	AGC	TTC	GTT	GGA	TCT	GGT	GAA	GGT	TCT	GGA	GGT	TTC	TGG	420
121	G	A	V	A	K	R	L	S	F	V	G	S	G	E	G	S	G	G	F	W	140
421	AAC	CGT	GGA	ATC	TCC	GCT	TGT	GCT	GTT	TGC	GAC	GGA	GCT	GCT	CCG	ATA	TTC	CGT	AAC	AAA	480
141	N	R	G	I	S	A	C	A	V	C	D	G	A	A	P	I	F	R	N	K	160
481	CCT	CTT	GCG	GTG	ATC	GGT	GGA	GGC	GAT	TCA	GCA	ATG	GAA	GAA	GCA	AAC	TTT	CTT	ACA	AAA	540
161	P	L	A	V	I	G	G	G	D	S	A	M	E	E	A	N	F	L	T	K	180
541	TAT	GGA	TCT	AAA	GTG	TAT	ATA	ATC	CAT	AGG	AGA	GAT	GCT	TTT	AGA	GCG	TCT	AAG	ATT	ATG	600
181	Y	G	S	K	V	Y	I	I	H	R	R	D	A	F	R	A	S	K	I	M	200
601	CAG	CAG	CGA	GCT	TTG	TCT	AAT	CCT	AAG	ATT	GAT	GTG	ATT	TGG	AAC	TCG	TCT	GTT	GTG	GAA	660
201	Q	Q	R	A	L	S	N	P	K	I	D	V	I	W	N	S	S	V	V	E	220
661	GCT	TAT	GGA	GAT	GGA	GAA	AGA	GAT	GTG	CTT	GGA	GGA	TTG	AAA	GTG	AAG	AAT	GTG	GTT	ACC	720
221	A	Y	G	D	G	E	R	D	V	L	G	G	L	K	V	K	N	V	V	T	240
721	GGA	GAT	GTT	TCT	GAT	TTA	AAA	GTT	TCT	GGA	TTG	TTC	TTT	GCT	ATT	GGT	CAT	GAG	CCA	GCT	780
241	G	D	V	S	D	L	K	V	S	G	L	F	F	A	I	G	H	E	P	A	260
781	ACC	AAG	TTT	TTG	GAT	GGT	GGT	GTT	GAG	TTA	GAT	TCG	GAT	GGT	TAT	GTT	GTC	ACG	AAG	CCT	840
261	T	K	F	L	D	G	G	V	E	L	D	S	D	G	Y	V	V	T	K	P	280
841	GGT	ACT	ACA	CAG	ACT	AGC	GTT	CCC	GGA	GTT	TTC	GCT	GCG	GGT	GAT	GTT	CAG	GAT	AAG	AAG	900
281	G	T	T	Q	T	S	V	P	G	V	F	A	A	G	D	V	Q	D	K	K	300
901	TAT	AGG	CAA	GCC	ATC	ACT	GCT	GCA	GGA	ACT	GGG	TGC	ATG	GCA	GCT	TTG	GAT	GCA	GAG	CAT	960
301	Y	R	Q	A	I	T	A	A	G	T	G	C	M	A	A	L	D	A	E	H	320
961	TAC	TTA	CAA	GAG	ATT	GGA	TCT	CAG	CAA	GGT	AAG	AGT	GAT	TGA							1002
321	Y	L	Q	E	I	G	S	Q	Q	G	K	S	D	*							334

FIGURE 11

ClustalW Formatted Alignments

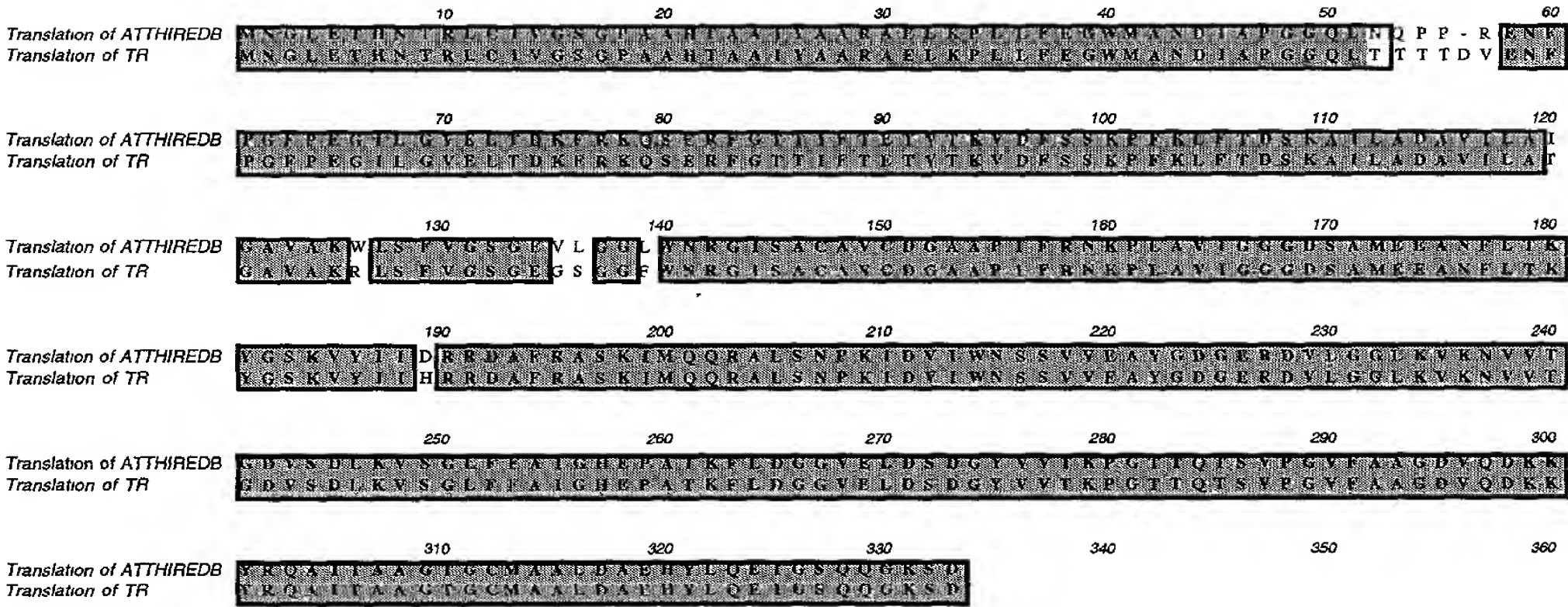


FIGURE 12

PstI

1 ctgcaggaattcattgtactcccagtatcattatagtgaaagtttggctctctcgccggtgggtttttacctctattta 80

81 aaggggttttccacctaaaaattctgggtatcattctcactttacttggtaactttaatttctcataatctttgggtgaaat 160

161 tatcacgcttccgcacacgatatccctacaaatttattatttggtaaacttttcaaaccgcataaaaattttatgaagtc 240

241 ccgtctatctttaatgtagtctaacttttcatattgaaatatataatttacttaatttttagcggttggtagaaagcataa 320

321 tgatttattcttattcttcttcatataaatgtttaatatataaataaaattctttaccttaagaaggatttcccat 400

401 tttatattttaaaaatatatttatcaaatatttttcaaccacgtaaactctcataataataagttgtttcaaaagtaataa 480

481 aatttaactccataatttttttattcgactgatcttaagcaacacccagtgacacaactagccatttttttctttgaat 560

561 aaaaaaatccaattatcattgtattttttttatataatgaaaatttcaccaaacaatcatttgtgggtatttctgaagcaa 640

641 gtcattgttatgcaaaattctataattcccatattgacactacggaagtaactgaagatctgcttttacatgagagacacat 720

721 cttctaaagtaattttaataatagttactatattcaagatttcatatatcaaatactcaatattacttctaaaaaattaa 800

801 ttagatataattaaaaatattacttttttaattttaagtttaattgttgaaattgtgactattgatttattattctactat 880

881 gtttaaattgttttatagatagtttaaagtaaataagtaagttagtagagtgttagagtgttacctaaaccataaac 960

961 tataagatttatgggtggactaattttcatatatattcttattgcttttaccttttcttggtatgtaagtccgtaactggaa 1040

1041 ttactgtgggttgccatggcactctgtgggtcttttgggtcatgcatggatgcttgcgcaagaaaaagacaaagaacaaag 1120

1121 aaaaaagacaaaacagagagacaaaacgcaatcacacaaccaactcaaattagtcactggctgatcaagatcgccgcgtc 1200

1201 catgtatgtctaaatgccatgcaaagcaacacgtgcttaacatgcactttaaatgggtcacccatctcaaccacacaca 1280

1281 aacacattgcctttttcttcatcatcaccacaaccacctgtatatattcattctcttccgccacctcaatttcttcactt 1360

1361 caacacacgtcaacctgcatatgcgtgtcatcccatgccaaatctccatgcatgttccaaccaccttctctcttatata 1440

1441 atacctataaatacctctaataatcactcacttctttcatcatccatccatccagagtactactactactataata 1520

1521 ccccaaccaactcatattcaataactactctact ATG GCT TCG GAA GAA GGA CAA GTG ATC GCC TGC 1587

1 M A S E E G Q V I A C 11

1588 CAC ACC GTT GAG ACA TGG AAC GAG CAG CTT CAG AAG GCT AAT GAA TCC AAA ACT CTT GTG 1647

12 H T V E T W N E Q L Q K A N E S K T L V 31

1648 GTG GTT GAT TTC ACG GCT TCT TGG TGT GGA CCA TGT CGT TTC ATC GCT CCA TTC TTT GCT 1707

32 V V D F T A S W C G P C R F I A P F F A 51

1708 GAT TTG GCT AAG AAA CTT CCT AAC GTG CTT TTC CTC AAG GTT GAT ACT GAT GAA TTG AAG 1767

52 D L A K K L P N V L F L K V D T D E L K 71

FIGURE 12 (CONT'D)

1768 TCG GTG GCA AGT GAT TGG GCG ATA CAG GCG ATG CCA ACC TTC ATG TTT TTG AAG GAA GGG 1827
72 S V A S D W A I Q A M P T F M F L K E G 91

1828 AAG ATT TTG GAC AAA GTT GTT GGA GCC AAG AAA GAT GAG CTT CAG TCT ACC ATT GCC AAA 1887
92 K I L D K V V G A K K D E L Q S T I A K 111
HindIII

1888 CAC TTG GCT TAA gcttaataagtatgaactaaaatgcatgtaggtgtaagagctcatggagagcatggaatattgt 1963
112 H L A * 115

1964 atccgaccatgtaacagtataataactgagctccatctcacttcttctatgaataaacaaggatggtatgatatttaa 2043

2044 cactctatctatgcaccttattgttctatgataaatttcctcttattattataaatcatctgaatcgtgacggcttatgg 2123

2124 aatgcttcaaatagtacaaaaacaatgtgtactataagactttctaaacaattctaacttttagcattgtgaacgagaca 2203

2204 taagtgttaagaagacataacaattataatggaagaagtttgtctccatttatattatattatattaccacttatgtatt 2283

2284 atattaggatgttaaggagacataacaattataaagagagaagtttgtatccatttatattatataactaccatttat 2363

2364 atattatacttatccacttatttaaatgtctttataagggttgatccatgatatttctaataatttttagttgatgtatat 2443

2444 gaaagggtactatttgaactctcttactctgtataaagggttgatcatccttaaagtgggtctatttaattttattgctt 2523

2524 cttacagataaaaaaaaaattatgagttgggttgataaaatattgaaggattttaaataataataataataataacat 2603

2604 ataatatatgtatataaatttattataatataacatttatctataaaaaagtaaatattgtcataaatctatacaatcgt 2683

2684 ttagccttgctggacgactctcaattattttaacgagagtaaacatatttgactttttggttatttaacaaattattatt 2763

2764 taacactatatgaaattttttttttttatcggcaaggaaataaaattaaattaggagggacaatgggtgtgtcccaatcct 2843

2844 tatacaaccaacttccacaggaagggtcaggtcggggacaacaaaaaacaggcaagggaattttttaatttgggttgctc 2923

2924 ttgtttgctgcataatttatgcagtaaaacactacacataacccttttagcagtagagcaatgggttgaccgtgtgcttag 3003

3004 cttcttttattttattttttttatcagcaaagaataaaataaaaatgagacacttcagggtatgtttcaacccttatac 3083

3084 aaaacccccaaaaacaagtttcctagcacccctaccaactaagggtacc 3129

KpnI

FIGURE 13

PstI

1 ctgcaggaattcattgtactcccagtatcattatagtgaaggttttggtctctctcgccggtggttttttacctctattta 80

81 aaggggttttccacctaaaaattctggtatcattctcactttacttggttactttaatttctcataatctttggttgaaat 160

161 tatcacgcttccgcacacgatatccctacaaatttattatttggttaaacattttcaaaccgcataaaaattttatgaagtc 240

241 ccgtctatctttaatgtagtctaacattttcatattgaaatatataatttacttaatttttagcggttggtagaagcataa 320

321 tgatttattcttattcttcttcatataaatgtttaatatataaacaattctttaccttaagaaggatttcccat 400

401 tttatattttaaaaatatatttatcaaataatttttcaaccacgtaaattctcataataataagttggttcaaagtaataa 480

481 aatttaactccataatttttttattcgactgatcttaagcaacaccagtgacacaactagccatttttttctttgaat 560

561 aaaaaatccaattatcattgtattttttttataacaatgaaaatttcaccaacaacatttgggtatttctgaagcaa 640

641 gtcattgttatgcaaaattctataattcccatttgacactacggaagtaactgaagatctgcttttacatgagacacat 720

721 cttctaaagtaattttaataatagttactatattcaagatttcataatcaataactcaatattacttctaaaaaattaa 800

801 ttagatataattaaaatattacttttttaattttaagtttaattggtgaatttggtgactattgatttattattctactat 880

881 gtttaaattgttttatagatagtttaaagtaaatataagtaatgtagtagagtgttagagtgtaccctaaaccataaac 960

961 tataagatttatggtggactaattttcatatatttcttattgcttttaccttttcttggtatgtaagtcgtaactggaa 1040

1041 ttactgtgggttgccatggcactctgtggtcttttggttcatgcatggatgcttgcgcaagaaaaagacaaagaacaaag 1120

1121 aaaaaagacaaaacagagagacaaaacgcaatcacacaaccaactcaaattagtcactggctgatcaagatcgccgcgtc 1200

1201 catgtatgtctaaatgccatgcaaagcaacacgtgcttaacatgcactttaaatggctcaccatctcaaccacacaca 1280

1281 aacacattgcctttttcttcatcatcaccacaaccacctgtatatattcattctcttccgccacctcaatttcttcactt 1360

1361 caacacacgtcaacctgcatatgcgtgtcatcccatgccc aaatctccatgcatgttccaaccaccttctctcttatata 1440

1441 atacctataaaatacctctaataatcactcacttctttcatcatccatccatccagagtactactactactataata 1520

1521 ccccaaccaactcatattcaataactactctact ATG GCG GAT ACA GCT AGA GGA ACC CAT CAC GAT 1587

1 M A D T A R G T H H D 11

1588 ATC ATC GGC AGA GAC CAG TAC CCG ATG ATG GGC CGA GAC CGA GAC CAG TAC CAG ATG TCC 1647

12 I I G R D Q Y P M M G R D R D Q Y Q M S 31

1648 GGA CGA GGA TCT GAC TAC TCC AAG TCT AGG CAG ATT GCT AAA GCT GCA ACT GCT GTC ACA 1707

32 G R G S D Y S K S R Q I A K A A T A V T 51

1708 GCT GGT GGT TCC CTC CTT GTT CTC TCC AGC CTT ACC CTT GTT GGA ACT GTC ATA GCT TTG 1767

52 A G G S L L V L S S L T L V G T V I A L 71

FIGURE 13 (CONT'D)

1768 ACT GTT GCA ACA CCT CTG CTC GTT ATC TTC AGC CCA ATC CTT GTC CCG GCT CTC ATC ACA 1827
72 T V A T P L L V I F S P I L V P A L I T 91

1828 GTT GCA CTC CTC ATC ACC GGT TTT CTT TCC TCT GGA GGG TTT GGC ATT GCC GCT ATA ACC 1887
92 V A L L I T G F L S S G G F G I A A I T 111

1888 GTT TTC TCT TGG ATT TAC AA *gtaagcacacatttatcatcttacttcataattttgtgcaatatgtgcatgca* 1960
112 V F S W I Y K 118

1961 *tgtgttgagccagtagcttttgatcaatttttttggtcgaataacaaatgtaacaataagaaattgcaaattctaggga* 2040

2041 *catttggttaactaaatacgaatttgacctagctagcttgaatgtgtctgtgtatatcatctatataggtaaaatgctt* 2120

2121 *ggtatgatacctattgattgtgaatag* G TAC GCA ACG GGA GAG CAC CCA CAG GGA TCA GAC AAG 2184
119 Y A T G E H P Q G S D K 130

2185 TTG GAC AGT GCA AGG ATG AAG TTG GGA AGC AAA GCT CAG GAT CTG AAA GAC AGA GCT CAG 2244
131 L D S A R M K L G S K A Q D L K D R A Q 150

2245 TAC TAC GGA CAG CAA CAT ACT GGT GGG GAA CAT GAC CGT GAC CGT ACT CGT GGT GGC CAG 2304
151 Y Y G Q Q H T G G E H D R D R T R G G Q 170

NcoI

2305 CAC ACT ACC ATG GCT TCG GAA GAA GGA CAA GTG ATC GCC TGC CAC ACC GTT GAG ACA TGG 2364
171 H T T M A S E E G Q V I A C H T V E T W 190

2365 AAC GAG CAG CTT CAG AAG GCT AAT GAA TCC AAA ACT CTT GTG GTG GTT GAT TTC ACG GCT 2424
191 N E Q L Q K A N E S K T L V V V D F T A 210

2425 TCT TGG TGT GGA CCA TGT CGT TTC ATC GCT CCA TTC TTT GCT GAT TTG GCT AAG AAA CTT 2484
211 S W C G P C R F I A P F F A D L A K K L 230

2485 CCT AAC GTG CTT TTC CTC AAG GTT GAT ACT GAT GAA TTG AAG TCG GTG GCA AGT GAT TGG 2544
231 P N V L F L K V D T D E L K S V A S D W 250

2545 GCG ATA CAG GCG ATG CCA ACC TTC ATG TTT TTG AAG GAA GGG AAG ATT TTG GAC AAA GTT 2604
251 A I Q A M P T F M F L K E G K I L D K V 270

2605 GTT GGA GCC AAG AAA GAT GAG CTT CAG TCT ACC ATT GCC AAA CAC TTG GCT TAA gcttaata 2666
271 V G A K K D E L Q S T I A K H L A * 288

2667 *agtatgaactaaaatgcatgtaggtgtaagagctcatggagagcatggaatattgtatccgaccatgtaacagtataata* 2746

2747 *actgagctccatctcacttcttctatgaataaacaaggatgttatgatataattaacactctatctatgcaccttattgt* 2826

2827 *tctatgataaatttcctcttattattataaatcatctgaatcgtgacggcttatggaatgcttcaaatagtacaaaaaca* 2906

2907 *aatgtgtactataagactttctaacaattctaacttttagcattgtgaacgagacataagtgttaagaagacataacaat* 2986

2987 *tataatggaagaagtttgtctccatttatattatattaccacttatgtattatattaggatgttaaggagacata* 3066

FIGURE 13 (CONT'D)

3067 acaattataaagagagaagtttgtatccatttatatatattatataactacccatttatatatattataacttatccacttattta 3146
3147 atgtctttataaggtttgatccatgatatttctaataatttttagttgatatgtatatgaaagggtactatttgaactctct 3226
3227 tactctgtataaaggttggatcatccttaaagtgggtctattttaattttattgcttcttacagataaaaaaaaaaattatg 3306
3307 agttggtttgataaaatattgaaggattttaaataataataataataataacatataatatgtatataaatttatt 3386
3387 ataataaacatttatctataaaaaagtaaatattgtcataaatctatacaatcgtttagccttgctggacgactctcaa 3466
3467 ttatttaaacgagagtaaacatatttgactttttggttatttaacaaattattatttaacactatatgaaattttttttt 3546
3547 tttatcggcaaggaaataaaattaaattaggaggggacaatggtgtgtcccaatccttatacaaccaacttccacaggaag 3626
3627 gtcaggtcggggacaacaaaaaacaggcaagggaattttttaatttgggttgtcttggttgctgcataatttatgcag 3706
3707 taaaacactacacataacccttttagcagtagagcaatggttgaccgtgtgcttagcttcttttattttatttttttatc 3786
3787 agcaaagaataaaataaaataaaatgagacacttcagggatgtttcaacccttatacaaaacccccaaaaacaagtttccta 3866
3867 gcaccctaccaactaaggtacc 3888

KpnI

FIGURE 14

PstI

1 ctgcaggaattcattgtactcccagtatcattatagtgaaagttttggctctctcgccggtgggttttttacctctattta 80

81 aaggggttttccacctaataattctgggtatcattctcactttacttggtactttaatttctcataatctttgggttgaaat 160

161 tatcacgcttccgcacacgatatccctacaaatttattatttggttaaacattttcaaaccgcataaaaattttatgaagtc 240

241 ccgtctatctttaatgtagtctaacattttcatattgaaatatataatttacttaatttttagcggttggtagaaagcataa 320

321 tgatttattcttattcttcttcatataaatgtttaatatatacaataataaacaattctttaccttaagaaggatttcccat 400

401 ttatatattttaaaaatatatttatcaaataatttttcaaccacgtaaattctcataataataagttgtttcaaaagtaataa 480

481 aatttaactccataatttttttattcgactgatcttaagcaacacccagtgacacaactagccatttttttctttgaat 560

561 aaaaaaatccaattatcattgtatttttttatacaatgaaaatttcaccaacaatcatttggtgatttctgaagcaa 640

641 gtcattgttatgcaaaattctataattcccatttgacactacggaagtaactgaagatctgcttttacatgcgagacacat 720

721 cttctaaagtaattttaataatagttactatattcaagatttcatatatcaaatactcaatattacttctaaaaaattaa 800

801 ttagatataattaaaaatattacttttttaattttaagtttaattggtgaatttggtgactattgatttattattctactat 880

881 gtttaaatgttttatagatagtttaagtaaatataagtaatgtagtagagtgttagagtgttacctaaccataaac 960

961 tataagatttatggtggactaattttcatatatatttcttattgcttttaccttttcttggtatgtaagtcgtaactggaa 1040

1041 ttactgtgggttgccatggcactctgtggtcttttggttcatgcatggatgcttgcgcaagaaaaagacaaagaacaaag 1120

1121 aaaaaagacaaaacagagagacaaaacgcaatcacacaaccaactcaaattagtcactggctgatcaagatcgccgcgtc 1200

1201 catgtatgtctaaatgccatgcaaagcaacacgtgcttaacatgcactttaaatggctcacccatctcaaccacacaca 1280

1281 aacacattgccttttttcttcatcatcaccacaaccacctgtatatattcattctcttccgccacctcaatttcttcaatt 1360

1361 caacacacgtcaacctgcatatgcgtgtcatcccatgcccgaatctccatgcatgttccaaccaccttctctcttatata 1440

1441 atacctataaataacctctaataatcactcacttctttcatcatccatccatccagagtactactactactataata 1520

1521 ccccaacccaactcatattcaataactactctact ATG GCT TCG GAA GAA GGA CAA GTG ATC GCC TGC 1587

1 M A S E E G Q V I A C 11

1588 CAC ACC GTT GAG ACA TGG AAC GAG CAG CTT CAG AAG GCT AAT GAA TCC AAA ACT CTT GTG 1647

12 H T V E T W N E Q L Q K A N E S K T L V 31

1648 GTG GTT GAT TTC ACG GCT TCT TGG TGT GGA CCA TGT CGT TTC ATC GCT CCA TTC TTT GCT 1707

32 V V D F T A S W C G P C R F I A P F F A 51

1708 GAT TTG GCT AAG AAA CTT CCT AAC GTG CTT TTC CTC AAG GTT GAT ACT GAT GAA TTG AAG 1767

52 D L A K K L P N V L F L K V D T D E L K 71

FIGURE 14 (CONT'D)

```
1768 TCG GTG GCA AGT GAT TGG GCG ATA CAG GCG ATG CCA ACC TTC ATG TTT TTG AAG GAA GGG 1827
    72 S V A S D W A I Q A M P T F M F L K E G 91

1828 AAG ATT TTG GAC AAA GTT GTT GGA GCC AAG AAA GAT GAG CTT CAG TCT ACC ATT GCC AAA 1887
    92 K I L D K V V G A K K D E L Q S T I A K 111

1888 CAC TTG GCT ATG GCG GAT ACA GCT AGA GGA ACC CAT CAC GAT ATC ATC GGC AGA GAC CAG 1947
    112 H L A M A D T A R G T H H D I I G R D Q 131

1948 TAC CCG ATG ATG GGC CGA GAC CGA GAC CAG TAC CAG ATG TCC GGA CGA GGA TCT GAC TAC 2007
    132 Y P M M G R D R D Q Y Q M S G R G S D Y 151

2008 TCC AAG TCT AGG CAG ATT GCT AAA GCT GCA ACT GCT GTC ACA GCT GGT GGT TCC CTC CTT 2067
    152 S K S R Q I A K A A T A V T A G G S L L 171

2068 GTT CTC TCC AGC CTT ACC CTT GTT GGA ACT GTC ATA GCT TTG ACT GTT GCA ACA CCT CTG 2127
    172 V L S S L T L V G T V I A L T V A T P L 191

2128 CTC GTT ATC TTC AGC CCA ATC CTT GTC CCG GCT CTC ATC ACA GTT GCA CTC CTC ATC ACC 2187
    192 L V I F S P I L V P A L I T V A L L I T 211

2188 GGT TTT CTT TCC TCT GGA GGG TTT GGC ATT GCC GCT ATA ACC GTT TTC TCT TGG ATT TAC 2247
    212 G F L S S G G F G I A A I T V F S W I Y 231

2248 AA gtaagcacacatttatcatcttacttcataatgtgtgcaatatgtgcatgcatgtgttgagccagtagctttggat 2326
    232 K 232

2327 caatgttttttggtcgaataacaaatgtaacaataagaaattgcaaattctaggggaacatttggttaactaaatacgaat 2406

2407 ttgacctagctagcttgaatgtgtctgtgtatatcatctatataggtaaaatgcttggtatgatacctattgattgtgaa 2486

2487 tag G TAC GCA ACG GGA GAG CAC CCA CAG GGA TCA GAC AAG TTG GAC AGT GCA AGG ATG 2544
    233 Y A T G E H P Q G S D K L D S A R M 250

2545 AAG TTG GGA AGC AAA GCT CAG GAT CTG AAA GAC AGA GCT CAG TAC TAC GGA CAG CAA CAT 2604
    251 K L G S K A Q D L K D R A Q Y Y G Q Q H 270

HindIII
2605 ACT GGT GGG GAA CAT GAC CGT GAC CGT ACT CGT GGT GGC CAG CAC ACT ACT TAA gcttgaata 2666
    271 T G G E H D R D R T R G G Q H T T * 288

2667 agtatgaactaaaatgcatgtaggtgtaagagctcatggagagcatggaatattgtatccgacctatgtaacagtataata 2746

2747 actgagctccatctcacttcttctatgaataaacaaggatgttatgatatattaacactctatctatgcaccttattgt 2826

2827 tctatgataaatttctcttattattataaatcatctgaatcgtgacggcttatggaatgcttcaaatagtacaaaaaca 2906

2907 aatgtgtactataagacttttctaaacaattctaacttttagcattgtgaacgagacataagtggttaagaagacataacaat 2986

2987 tataatggaagaagtttgtctccatttatatatattatattacccacttatgtattatattaggatgttaaggagacata 3066
```

FIGURE 14 (CONT'D)

3067 acaattataaagagagaagtttgtatccatttatatatattatataactacccatttatatatattataacttatccacttattta 3146
3147 atgtctttataaggtttgatccatgatatttctaataatttttagttgatatgtatatgaaaggtactatttgaactctct 3226
3227 tactctgtataaaggttggatcatccttaaagtgggtctattttaattttattgcttcttacagataaaaaaaaaaattatg 3306
3307 agttggtttgataaaatattgaaggattttaaataataataaataaataacatataatataatgtatataaatttatt 3386
3387 ataataaacatttatctataaaaaagtaaataattgtcataaatctataacaatcgtttagccttgctggacgactctcaa 3466
3467 ttattttaaacgagagtaaacaatatttgactttttggttattttaacaaattattatttaacactatatgaaattttttttt 3546
3547 tttatcggcaaggaaataaaaattaaattaggaggggacaatggtgtgtcccaatccttataacaaccaacttccacaggaag 3626
3627 gtcaggtcggggacaacaaaaaacaggcaagggaattttttaatttgggttgctcttgcttgctgcataatttatgcag 3706
3707 taaaacactacacataacccttttagcagtagagcaatggttgaccgtgtgcttagcttcttttattttatttttttatc 3786
3787 agcaaagaataaataaaaataaaaatgagacacttcagggatgtttcaacccttatacaaaacccccaaaaacaagtttccta 3866
3867 gcaccctaccaactaaggtacc 3888

KpnI

FIGURE 15

PstI

1 ctgcaggaatttcattgtactcccagtatcattatagtgaaagttttggctctctcgccgggtgggttttttacctctattta 80

81 aaggggttttccacctaataattctgggtatcattctcactttacttggtactttaattttctcataatctttgggtgaaat 160

161 tatcacgcttccgcacacgatatccctacaaatttattatttggttaaaccattttcaaaccgcataaaattttatgaagtc 240

241 ccgtctatctttaatgtagtctaaccattttcatattgaaatatataatttacttaatttttagcggttggtagaaagcataa 320

321 tgattttattcttattcttcttcatataaatgtttaatatatacaataataaacaattctttaccttaagaaggatttcccat 400

401 tttatatttttaaaaatatatttatcaaataatttttcaaccacgtaaattctcataataataagttgtttcaaaagtaataa 480

481 aatttaactccataattttttttattcgactgatcttaagcaacacccagtgacacaactagccattttttctttgaat 560

561 aaaaaaatccaattatcattgtattttttttatacaatgaaaatttcaccaaacaatcatttggtggtattttctgaagcaa 640

641 gtcattgttatgcaaaattctataattcccatttgacactacggaagtaactgaagatctgctttttacatgcgagacacat 720

721 cttctaaagtaatttttaataatagttactatattcaagatttcatatatcaaatactcaatattacttctaaaaaattaa 800

801 ttagatataattaaaaatattactttttttaattttaagtttaattggtgaatttggtgactattgatttattattctactat 880

881 gtttaaatggttttatagatagtttaagtaaatataagtaatgtagtagagtgttagagtgttacctaaccataaac 960

961 tataagatttatggtggactaattttcatatatttcttattgcttttaccttttcttggtatgtaagtcgtaactggaa 1040

1041 ttactgtgggttgccatggcactctgtggtcttttggttcatgcatggatgcttgcgcaagaaaaagacaaagaacaaag 1120

1121 aaaaaagacaaaacagagagacaaaacgcaatcacacaaccaactcaaattagtcactggctgatcaagatcgccgcgctc 1200

1201 catgtatgtctaaatgccatgcaaagcaacacgtgcttaacatgcacttttaaatggctcacccatctcaaccacacaca 1280

1281 aacacattgcctttttcttcatcatcaccacaaccacctgtatatattcattctcttccgccacctcaatttcttcactt 1360

1361 caacacacgtcaacctgcatatgcgtgtcatcccatgccccaaatctccatgcatgttccaaccaccttctctcttatata 1440

1441 atacctataaaatacctctaataatcactcacttctttcatcatccatccatccagagtactactactctactactataata 1520

1521 ccccaaccaactcatattcaatactactctact ATG AAT GGT CTC GAA ACT CAC AAC ACA AGG CTC 1587

1 M N G L E T H N T R L 11

1588 TGT ATC GTA GGA AGT GGC CCA GCG GCA CAC ACG GCG GCG ATT TAC GCA GCT AGG GCT GAA 1647

12 C I V G S G P A A H T A A I Y A A R A E 31

1648 CTT AAA CCT CTT CTC TTC GAA GGA TGG ATG GCT AAC GAC ATC GCT CCC GGT GGT CAA CTA 1707

32 L K P L L F E G W M A N D I A P G G Q L 51

1708 ACA ACC ACC ACC GAC GTC GAG AAT TTC CCC GGA TTT CCA GAA GGT ATT CTC GGA GTA GAG 1767

52 T T T T D V E N F P G F P E G I L G V E 71

FIGURE 15 (CONT'D)

1768 CTC ACT GAC AAA TTC CGT AAA CAA TCG GAG CGA TTC GGT ACT ACG ATA TTT ACA GAG ACG 1827
72 L T D K F R K Q S E R F G T T I F T E T 91

1828 GTG ACG AAA GTC GAT TTC TCT TCG AAA CCG TTT AAG CTA TTC ACA GAT TCA AAA GCC ATT 1887
92 V T K V D F S S K P F K L F T D S K A I 111

1888 CTC GCT GAC GCT GTG ATT CTC GCT ACT GGA GCT GTG GCT AAG CGG CTT AGC TTC GTT GGA 1947
112 L A D A V I L A T G A V A K R L S F V G 131

1948 TCT GGT GAA GGT TCT GGA GGT TTC TGG AAC CGT GGA ATC TCC GCT TGT GCT GTT TGC GAC 2007
132 S G E G S G G F W N R G I S A C A V C D 151

2008 GGA GCT GCT CCG ATA TTC CGT AAC AAA CCT CTT GCG GTG ATC GGT GGA GGC GAT TCA GCA 2067
152 G A A P I F R N K P L A V I G G G D S A 171

2068 ATG GAA GAA GCA AAC TTT CTT ACA AAA TAT GGA TCT AAA GTG TAT ATA ATC CAT AGG AGA 2127
172 M E E A N F L T K Y G S K V Y I I H R R 191

2128 GAT GCT TTT AGA GCG TCT AAG ATT ATG CAG CAG CGA GCT TTG TCT AAT CCT AAG ATT GAT 2187
192 D A F R A S K I M Q Q R A L S N P K I D 211

2188 GTG ATT TGG AAC TCG TCT GTT GTG GAA GCT TAT GGA GAT GGA GAA AGA GAT GTG CTT GGA 2247
212 V I W N S S V V E A Y G D G E R D V L G 231

2248 GGA TTG AAA GTG AAG AAT GTG GTT ACC GGA GAT GTT TCT GAT TTA AAA GTT TCT GGA TTG 2307
232 G L K V K N V V T G D V S D L K V S G L 251

2308 TTC TTT GCT ATT GGT CAT GAG CCA GCT ACC AAG TTT TTG GAT GGT GGT GTT GAG TTA GAT 2367
252 F F A I G H E P A T K F L D G G V E L D 271

2368 TCG GAT GGT TAT GTT GTC ACG AAG CCT GGT ACT ACA CAG ACT AGC GTT CCC GGA GTT TTC 2427
272 S D G Y V V T K P G T T Q T S V P G V F 291

2428 GCT GCG GGT GAT GTT CAG GAT AAG AAG TAT AGG CAA GCC ATC ACT GCT GCA GGA ACT GGG 2487
292 A A G D V Q D K K Y R Q A I T A A G T G 311

2488 TGC ATG GCA GCT TTG GAT GCA GAG CAT TAC TTA CAA GAG ATT GGA TCT CAG CAA GGT AAG 2547
312 C M A A L D A E H Y L Q E I G S Q Q G K 331

2548 AGT GAT TGA agcttaataagtatgaactaaaatgcatgtaggtgtaagagctcatggagagcatggaatattgtatc 2624
332 S D * HindIII 334

2625 cgaccatgtaacagtataataactgagctccatctcacttcttctatgaataaacaaggatgttatgatatattaacac 2704

2705 tctatctatgcaccttattgttctatgataaatttctcttattattataaatcatctgaatcgtgacggccttatggaat 2784

2785 gcttcaaatagtacaaaaacaatgtgtactataagacttttctaaacaattctaacttttagcattgtgaacgagacataa 2864

2865 gtgttaagaagacataacaattataatggaagaagtttgtctccatttatattatattatattaccacttatgtattata 2944

FIGURE 15 (CONT'D)

2945 ttaggatgttaaggagacataacaattataaagagagaagtttgatccatttatatattatataactacccatttatata 3024
3025 ttatacttatccacttattttaatgtctttataaggtttgatccatgatatttctaataatttttagttgatatgtatatgaa 3104
3105 aggggtactatttgaactctcttactctgtataaaggttggatcatccttaaagtgggtctattttaattttattgcttctt 3184
3185 acagataaaaaaaaaattatgagttggtttgataaaatattgaaggatttaaaataataataaataaataaacatata 3264
3265 atatatgtatataaattttattataataaacatttatctataaaaaagtaaataattgtcataaatctatacaatcgttta 3344
3345 gccttgctggacgactctcaattattttaaacgagagtaaacatatttgactttttggttattttaacaaattattatttaa 3424
3425 cactatatgaaatttttttttttttatcggcaaggaaataaaattaaattaggagggacaatgggtgtgtcccaatccttat 3504
3505 acaaccaacttccacaggaagggtcaggtcggggacaacaaaaaacaggcaagggaattttttaatttggggtgtcttg 3584
3585 tttgctgcataatttatgcagtaaaacactacacataacccttttagcagtagagcaatgggttgaccgtgtgcttagctt 3664
3665 cttttattttatttttttttatcagcaaagaataaaataaaataaaatgagacacttcagggatgtttcaacccttatataaaa 3744
3745 accccaaaaacaagtttcctagcaccctaccaactaaggtacc 3787

KpnI

FIGURE 16

PstI

1 ctgcaggaattcattgtactcccagtatcattatagtgaagttttggctctctcgccggtgggttttttacctctattta 80

81 aagggggtttccacctaataattctgggtatcattctcactttacttggtactttaatttctcataatctttgggtgaaat 160

161 tatcacgcttccgcacacgatatccctacaaatttattatttggttaaacattttcaaaccgcataaaattttatgaagtc 240

241 ccgtctatctttaatgtagtctaacattttcatattgaaatatataatttacttaatttttagcgttggttagaaagcataa 320

321 tgatttattcttattcttcttcatataaatgtttaatatataataaacaattctttaccttaagaaggatttcccat 400

401 tttatatttttaaaaatatatttatcaaataatttttcaaccacgtaaattctcataataataagttgtttcaaaagtaataa 480

481 aatttaactccataatttttttattcgactgatcttaaagcaacacccagtgacacaactagccattttttctttgaat 560

561 aaaaaaatccaattatcattgtattttttttatataaatgaaaatttcaccaacaacattttgtgggtattttctgaagcaa 640

641 gtcattgttatgcaaaattctataattcccatttgacactacggaagtaactgaagatctgcttttacatgcgagacacat 720

721 cttctaaagtaattttaataatagttactatattcaagatttcatatatcaaatactcaatattacttctaaaaaattaa 800

801 ttagatataattaaaaatattacttttttaattttaagtttaattgttggaattttgtgactattgatttattattctactat 880

881 gtttaaatgtttttatagatagtttaagtaaatataagtaatgtagtagagtgttagagtgttaccctaaaccataaac 960

961 tataagatttatgggtggactaattttcatatatttcttattgcttttaccttttcttggtatgtaagtcgtaactggaa 1040

1041 ttactgtggggttgccatggcactctgtggtcttttggttcatgcatggatgcttgcgcaagaaaaagacaaagaacaaag 1120

1121 aaaaaagacaaaacagagagacaaaacgcaatcacacaaccaactcaaattagtcactggctgatcaagatcgccgcgctc 1200

1201 catgtatgtctaaatgccatgcaaagcaacacgtgcttaacatgcactttaaatggctcaccatctcaaccacacaca 1280

1281 aacacattgcctttttcttcatcatcaccacaaccacctgtatatattcattctcttccgccacctcaatttcttcactt 1360

1361 caacacacgtcaacctgcatatgcgtgtcatcccatgccc aaatctccatgcatgttccaaccaccttctctcttatata 1440

1441 atacctataaatacctctaataatcactcacttctttcatcatccatccatccagagtactactactctactactataata 1520

1521 ccccaaccaactcatattcaatactactctact ATG GCG GAT ACA GCT AGA GGA ACC CAT CAC GAT 1587

1 M A D T A R G T H H D 11

1588 ATC ATC GGC AGA GAC CAG TAC CCG ATG ATG GGC CGA GAC CGA GAC CAG TAC CAG ATG TCC 1647

12 I I G R D Q Y P M M G R D R D Q Y Q M S 31

1648 GGA CGA GGA TCT GAC TAC TCC AAG TCT AGG CAG ATT GCT AAA GCT GCA ACT GCT GTC ACA 1707

32 G R G S D Y S K S R Q I A K A A T A V T 51

1708 GCT GGT GGT TCC CTC CTT GTT CTC TCC AGC CTT ACC CTT GTT GGA ACT GTC ATA GCT TTG 1767

FIGURE 16 (CONT'D)

52 A G G S L L V L S S L T L V G T V I A L 71

1768 ACT GTT GCA ACA CCT CTG CTC GTT ATC TTC AGC CCA ATC CTT GTC CCG GCT CTC ATC ACA 1827
72 T V A T P L L V I F S P I L V P A L I T 91

1828 GTT GCA CTC CTC ATC ACC GGT TTT CTT TCC TCT GGA GGG TTT GGC ATT GCC GCT ATA ACC 1887
92 V A L L I T G F L S S G G F G I A A I T 111

1888 GTT TTC TCT TGG ATT TAC AA *gtaagcacacatttatcatcttactttcataattttgtgcaatatgtgcatgca* 1960
112 V F S W I Y K 118

1961 *tgtgttgagccagtagcctttggatcaattttttggtcgaataacaaatgtaacaataagaaattgcaaattctagggaa* 2040

2041 *catttgggttaactaaatacgaaatttgacctagctagcttgaatgtgtctgtgtatatcatctatataggtaaaatgctt* 2120

2121 *ggtatgatacctattgattgtgaatag* G TAC GCA ACG GGA GAG CAC CCA CAG GGA TCA GAC AAG 2184
119 Y A T G E H P Q G S D K 130

2185 TTG GAC AGT GCA AGG ATG AAG TTG GGA AGC AAA GCT CAG GAT CTG AAA GAC AGA GCT CAG 2244
131 L D S A R M K L G S K A Q D L K D R A Q 150

2245 TAC TAC GGA CAG CAA CAT ACT GGT GGG GAA CAT GAC CGT GAC CGT ACT CGT GGT GGC CAG 2304
151 Y Y G Q Q H T G G E H D R D R T R G G Q 170

2305 CAC ACT ACC ATG AAT GGT CTC GAA ACT CAC AAC ACA AGG CTC TGT ATC GTA GGA AGT GGC 2364
171 H T T M N G L E T H N T R L C I V G S G 190

2365 CCA GCG GCA CAC ACG GCG GCG ATT TAC GCA GCT AGG GCT GAA CTT AAA CCT CTT CTC TTC 2424
191 P A A H T A A I Y A A R A E L K P L L F 210

2425 GAA GGA TGG ATG GCT AAC GAC ATC GCT CCC GGT GGT CAA CTA ACA ACC ACC ACC GAC GTC 2484
211 E G W M A N D I A P G G Q L T T T T D V 230

2485 GAG AAT TTC CCC GGA TTT CCA GAA GGT ATT CTC GGA GTA GAG CTC ACT GAC AAA TTC CGT 2544
231 E N F P G F P E G I L G V E L T D K F R 250

2545 AAA CAA TCG GAG CGA TTC GGT ACT ACG ATA TTT ACA GAG ACG GTG ACG AAA GTC GAT TTC 2604
251 K Q S E R F G T T I F T E T V T K V D F 270

2605 TCT TCG AAA CCG TTT AAG CTA TTC ACA GAT TCA AAA GCC ATT CTC GCT GAC GCT GTG ATT 2664
271 S S K P F K L F T D S K A I L A D A V I 290

2665 CTC GCT ACT GGA GCT GTG GCT AAG CGG CTT AGC TTC GTT GGA TCT GGT GAA GGT TCT GGA 2724
291 L A T G A V A K R L S F V G S G E G S G 310

2725 GGT TTC TGG AAC CGT GGA ATC TCC GCT TGT GCT GTT TGC GAC GGA GCT GCT CCG ATA TTC 2784
311 G F W N R G I S A C A V C D G A A P I F 330

2785 CGT AAC AAA CCT CTT GCG GTG ATC GGT GGA GGC GAT TCA GCA ATG GAA GAA GCA AAC TTT 2844
331 R N K P L A V I G G G D S A M E E A N F 350

FIGURE 16 (CONT'D)

2845 CTT ACA AAA TAT GGA TCT AAA GTG TAT ATA ATC CAT AGG AGA GAT GCT TTT AGA GCG TCT 2904
351 L T K Y G S K V Y I I H R R D A F R A S 370

2905 AAG ATT ATG CAG CAG CGA GCT TTG TCT AAT CCT AAG ATT GAT GTG ATT TGG AAC TCG TCT 2964
371 K I M Q Q R A L S N P K I D V I W N S S 390

2965 GTT GTG GAA GCT TAT GGA GAT GGA GAA AGA GAT GTG CTT GGA GGA TTG AAA GTG AAG AAT 3024
391 V V E A Y G D G E R D V L G G L K V K N 410

3025 GTG GTT ACC GGA GAT GTT TCT GAT TTA AAA GTT TCT GGA TTG TTC TTT GCT ATT GGT CAT 3084
411 V V T G D V S D L K V S G L F F A I G H 430

3085 GAG CCA GCT ACC AAG TTT TTG GAT GGT GGT GTT GAG TTA GAT TCG GAT GGT TAT GTT GTC 3144
431 E P A T K F L D G G V E L D S D G Y V V 450

3145 ACG AAG CCT GGT ACT ACA CAG ACT AGC GTT CCC GGA GTT TTC GCT GCG GGT GAT GTT CAG 3204
451 T K P G T T Q T S V P G V F A A G D V Q 470

3205 GAT AAG AAG TAT AGG CAA GCC ATC ACT GCT GCA GGA ACT GGG TGC ATG GCA GCT TTG GAT 3264
471 D K K Y R Q A I T A A G T G C M A A L D 490

3265 GCA GAG CAT TAC TTA CAA GAG ATT GGA TCT CAG CAA GGT AAG AGT GAT TGA agcttaataagt 3327
491 A E H Y L Q E I G S Q Q G K S D * HindIII 507

3328 atgaactaaaatgcatgtaggtgtaagagctcatggagagcatggaatattgtatccgaccatgtaacagtataataact 3407

3408 gagctccatctcacttcttctatgaataaacaaggatgttatgatataattaacactctatctatgcaccttattgttct 3487

3488 atgataaatttctcttattattataaatcatctgaatcgtgacggcttatggaatgcttcaaatagtacaaaaacaaat 3567

3568 gtgtactataagacttttctaaacaatttctaacttttagcattgtgaacgagacataagtgttaagaagacataacaattat 3647

3648 aatggaagaagtttgtctccatttatatattatataactaccacttatgtattatattaggatgttaaggagacataaca 3727

3728 attataaagagagaagtttgtatccatttatatattatataactaccacttatatattatacttatccacttatttaagt 3807

3808 tctttataaggtttgatccatgatatttctaataatttttagttgatatgtatatgaaaggggtactatttgaactctcttac 3887

3888 tctgtataaaggttgatcatccttaagtggtctattttaattttattgcttcttacagataaaaaaaaaaattatgagt 3967

3968 tggtttgataaaatattgaaggatttaaaataataaataaataaataacatataatataatgtatataaatttattata 4047

4048 atataacatttatctataaaaaagtaaatattgtcataaatctatacaatcgtttagccttgctggacgactctcaatta 4127

4128 tttaaacgagagtaaacatatttgacttttttggttatttaacaaattattatttaacactatatgaaattttttttttt 4207

4208 atcggcaaggaaataaaattaaattaggagggacaatggtgtgtcccaatccttataacaaccaacttccacaggaaggtc 4287

KpnI

FIGURE 17

PstI

1 ctgcaggaattcattgtactcccagtatcattatagtgaaagttttggctctctcgccgggtgggttttttacctctattta 80

81 aaggggttttccacctaataattctggtatcattctcactttacttggtactttaatttctcataatctttggttgaaat 160

161 tatcacgcttccgcacacgatatccctacaaatttattatttgttaaacattttcaaaccgcataaaattttatgaagtc 240

241 ccgtctatctttaatgtagtctaacattttcatattgaaatatataatttacttaatttttagcggttggtagaagcataa 320

321 tgattttattcttattcttcttcatataaatgtttaatatatacaataataaacaattctttaccttaagaaggatttcccat 400

401 tttatattttaaaaaatataatttatcaaataatttttcaaccacgtaaattctcataataataagttgtttcaaaagtaataa 480

481 aattttaactccataatttttttattcgactgatcttaagcaacacccagtgacacaactagccatttttttctttgaat 560

561 aaaaaaatccaattatcattgtattttttttatacaatgaaaatttcaccaaacaatcatttgtggtatttctgaagcaa 640

641 gtcattgttatgcaaaattctataatttccatttgacactacggaagtaactgaagatctgcttttacatgagagacacat 720

721 cttctaaagtaattttaataatagttactatattcaagatttcatatatcaaatactcaatattacttctaaaaaattaa 800

801 ttagatataattaaaaatattacttttttaattttaagtttaattgttgactattgatttattattctactat 880

881 gtttaaatgttttatagatagtttaagtaaatataagtaatgtagtagagtgttagagtgttaccctaaaccataaac 960

961 tataagatttatggtggactaattttcatatatttcttattgcttttaccttttcttggtatgtaagtcgtaactggaa 1040

1041 ttactgtgggttgccatggcactctgtggtcttttggttcatgcatggatgcttgcgcaagaaaaagacaaagaacaaag 1120

1121 aaaaaagacaaaacagagagacaaaacgcaatcacacaaccaactcaaattagtcactggctgatcaagatcgccgcgtc 1200

1201 catgtatgtctaaatgccatgcaaagcaacacgtgcttaacatgcactttaaatggctcacccatctcaaccacacaca 1280

1281 aacacattgcctttttcttcatcatcaccacaaccacctgtatatattcattctcttccgccacctcaatttcttcactt 1360

1361 caacacacgtcaacctgcatatgcgtgtcatcccatgccc aaatctccatgcatgttccaaccaccttctcttataata 1440

1441 atacctataaataccttctaataatcactcacttctttcatcatccatccatccagagtactactactctactataata 1520

1521 ccccaacccaactcatattcaatactactctact ATG AAT GGT CTC GAA ACT CAC AAC ACA AGG CTC 1587

1 M N G L E T H N T R L 11

1588 TGT ATC GTA GGA AGT GGC CCA GCG GCA CAC ACG GCG GCG ATT TAC GCA GCT AGG GCT GAA 1647

12 C I V G S G P A A H T A A I Y A A R A E 31

1648 CTT AAA CCT CTT CTC TTC GAA GGA TGG ATG GCT AAC GAC ATC GCT CCC GGT GGT CAA CTA 1707

32 L K P L L F E G W M A N D I A P G G Q L 51

1708 ACA ACC ACC ACC GAC GTC GAG AAT TTC CCC GGA TTT CCA GAA GGT ATT CTC GGA GTA GAG 1767

52 T T T T D V E N F P G F P E G I L G V E 71

FIGURE 17 (CONT'D)

1768	CTC	ACT	GAC	AAA	TTC	CGT	AAA	CAA	TCG	GAG	CGA	TTC	GGT	ACT	ACG	ATA	TTT	ACA	GAG	ACG	1827
72	L	T	D	K	F	R	K	Q	S	E	R	F	G	T	T	I	F	T	E	T	91
1828	GTG	ACG	AAA	GTC	GAT	TTC	TCT	TCG	AAA	CCG	TTT	AAG	CTA	TTC	ACA	GAT	TCA	AAA	GCC	ATT	1887
92	V	T	K	V	D	F	S	S	K	P	F	K	L	F	T	D	S	K	A	I	111
1888	CTC	GCT	GAC	GCT	GTG	ATT	CTC	GCT	ACT	GGA	GCT	GTG	GCT	AAG	CGG	CTT	AGC	TTC	GTT	GGA	1947
112	L	A	D	A	V	I	L	A	T	G	A	V	A	K	R	L	S	F	V	G	131
1948	TCT	GGT	GAA	GGT	TCT	GGA	GGT	TTC	TGG	AAC	CGT	GGA	ATC	TCC	GCT	TGT	GCT	GTT	TGC	GAC	2007
132	S	G	E	G	S	G	G	F	W	N	R	G	I	S	A	C	A	V	C	D	151
2008	GGA	GCT	GCT	CCG	ATA	TTC	CGT	AAC	AAA	CCT	CTT	GCG	GTG	ATC	GGT	GGA	GGC	GAT	TCA	GCA	2067
152	G	A	A	P	I	F	R	N	K	P	L	A	V	I	G	G	G	D	S	A	171
2068	ATG	GAA	GAA	GCA	AAC	TTT	CTT	ACA	AAA	TAT	GGA	TCT	AAA	GTG	TAT	ATA	ATC	CAT	AGG	AGA	2127
172	M	E	E	A	N	F	L	T	K	Y	G	S	K	V	Y	I	I	H	R	R	191
2128	GAT	GCT	TTT	AGA	GCG	TCT	AAG	ATT	ATG	CAG	CAG	CGA	GCT	TTG	TCT	AAT	CCT	AAG	ATT	GAT	2187
192	D	A	F	R	A	S	K	I	M	Q	Q	R	A	L	S	N	P	K	I	D	211
2188	GTG	ATT	TGG	AAC	TCG	TCT	GTT	GTG	GAA	GCT	TAT	GGA	GAT	GGA	GAA	AGA	GAT	GTG	CTT	GGA	2247
212	V	I	W	N	S	S	V	V	E	A	Y	G	D	G	E	R	D	V	L	G	231
2248	GGA	TTG	AAA	GTG	AAG	AAT	GTG	GTT	ACC	GGA	GAT	GTT	TCT	GAT	TTA	AAA	GTT	TCT	GGA	TTG	2307
232	G	L	K	V	K	N	V	V	T	G	D	V	S	D	L	K	V	S	G	L	251
2308	TTC	TTT	GCT	ATT	GGT	CAT	GAG	CCA	GCT	ACC	AAG	TTT	TTG	GAT	GGT	GGT	GTT	GAG	TTA	GAT	2367
252	F	F	A	I	G	H	E	P	A	T	K	F	L	D	G	G	V	E	L	D	271
2368	TCG	GAT	GGT	TAT	GTT	GTC	ACG	AAG	CCT	GGT	ACT	ACA	CAG	ACT	AGC	GTT	CCC	GGA	GTT	TTC	2427
272	S	D	G	Y	V	V	T	K	P	G	T	T	Q	T	S	V	P	G	V	F	291
2428	GCT	GCG	GGT	GAT	GTT	CAG	GAT	AAG	AAG	TAT	AGG	CAA	GCC	ATC	ACT	GCT	GCA	GGA	ACT	GGG	2487
292	A	A	G	D	V	Q	D	K	K	Y	R	Q	A	I	T	A	A	G	T	G	311
2488	TGC	ATG	GCA	GCT	TTG	GAT	GCA	GAG	CAT	TAC	TTA	CAA	GAG	ATT	GGA	TCT	CAG	CAA	GGT	AAG	2547
312	C	M	A	A	L	D	A	E	H	Y	L	Q	E	I	G	S	Q	Q	G	K	331
2548	AGT	GAT	ATG	GCG	GAT	ACA	GCT	AGA	GGA	ACC	CAT	CAC	GAT	ATC	ATC	GGC	AGA	GAC	CAG	TAC	2607
332	S	D	M	A	D	T	A	R	G	T	H	H	D	I	I	G	R	D	Q	Y	351
2608	CCG	ATG	ATG	GGC	CGA	GAC	CGA	GAC	CAG	TAC	CAG	ATG	TCC	GGA	CGA	GGA	TCT	GAC	TAC	TCC	2667
352	P	M	M	G	R	D	R	D	Q	Y	Q	M	S	G	R	G	S	D	Y	S	371
2668	AAG	TCT	AGG	CAG	ATT	GCT	AAA	GCT	GCA	ACT	GCT	GTC	ACA	GCT	GGT	GGT	TCC	CTC	CTT	GTT	2727
372	K	S	R	Q	I	A	K	A	A	T	A	V	T	A	G	G	S	L	L	V	391

FIGURE 17 (CONT'D)

2728 CTC TCC AGC CTT ACC CTT GTT GGA ACT GTC ATA GCT TTG ACT GTT GCA ACA CCT CTG CTC 2787
392 L S S L T L V G T V I A L T V A T P L L 411

2788 GTT ATC TTC AGC CCA ATC CTT GTC CCG GCT CTC ATC ACA GTT GCA CTC CTC ATC ACC GGT 2847
412 V I F S P I L V P A L I T V A L L I T G 431

2848 TTT CTT TCC TCT GGA GGG TTT GGC ATT GCC GCT ATA ACC GTT TTC TCT TGG ATT TAC AA g 2907
432 F L S S G G F G I A A I T V F S W I Y K 451

2908 *taagcacacatTTtatcatcttactttcataatTTTTgtgcaatatgtgcatgcatgtgttgagccagtagctttggatcaat* 2987

2988 *TTTTTggTcgaataacaaatgtaacaataagaaattgcaaattctaggggaacatttggTTaactaaatacgaatttga* 3067

3068 *cctagctagcttgaatgtgtctgtgtatatcatctatataggtaaaatgcttggTatgatacctattgattgtgaatag* 3146

3147 G TAC GCA ACG GGA GAG CAC CCA CAG GGA TCA GAC AAG TTG GAC AGT GCA AGG ATG AAG 3204
452 Y A T G E H P Q G S D K L D S A R M K 470

3205 TTG GGA AGC AAA GCT CAG GAT CTG AAA GAC AGA GCT CAG TAC TAC GGA CAG CAA CAT ACT 3264
471 L G S K A Q D L K D R A Q Y Y G Q Q H T 490

3265 GGT GGG GAA CAT GAC CGT GAC CGT ACT CGT GGT GGC CAG CAC ACT ACT TAA gcttaataagta 3327
491 G G E H D R D R T R G G Q H T T * HindIII 507

3328 *tgaactaaaatgcatgtaggtgtaagagctcatggagagcatggaatattgtatccgaccatgtaacagtataataactg* 3407

3408 *agctccatctcacttcttctatgaataaacaaggatgttatgatataattaacactctatctatgcaccttattgttcta* 3487

3488 *tgataaatttctcttattattataaatcatctgaatcgTgacggcttatggaatgcttcaaatagtacaaaaacaaatg* 3567

3568 *tgtactataagacttttctaacaattctaacttttagcattgtgaacgagacataagtgttaagaagacataacaattata* 3647

3648 *atggaagaagtttgtctccatttatatatattatattaccacttatgtattatattaggatgttaaggagacataacaa* 3727

3728 *ttataaagagagaagtttgtatccatttatatatataactaccactttatatattataacttatccacttattttaatgt* 3807

3808 *ctttataaggtttgatccatgatatttctaataatttttagttgatatgtatatgaaagggTactatttgaactctcttact* 3887

3888 *ctgtataaaggTtgatcatccttaaagTgggtctattttaattttattgcttcttacagataaaaaaaaaaattatgagtt* 3967

3968 *ggtttgataaaaatattgaaggattttaaataataataataataataacatataatatgtatataaatttattataa* 4047

4048 *tataacatttatctataaaaaagTaaatattgtcataaatctatacaatcgTtttagccttgctggacgactctcaattat* 4127

4128 *ttaaacgagagTaaacatatttgactttttggTtatttaacaaattattatttaacactatatgaaatttttttttttta* 4207

4208 *tcggcaaggaaataaaaattaaattaggaggTgacaatggTgtgtcccaatccttatacaaccaacttccacaggaaggTca* 4287

FIGURE 17 (CONT'D)

4288 ggtcggggacaacaaaaaacagggaagggaattttttaatttgggttggtcttggttgctgcataatttatgcagtaaa 4367
4368 acactacacataacccttttagcagtagagcaatggttgaccgtgtgcttagcttcttttattttatttttttatcagca 4447
4448 aagaataaataaaaataaaaatgagacacttcagggatgtttcaacccttatacaaaacccccaaaaacaagtttcctagcac 4527
4528 cctaccaactaaggtacc 4545

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FIGURE 18

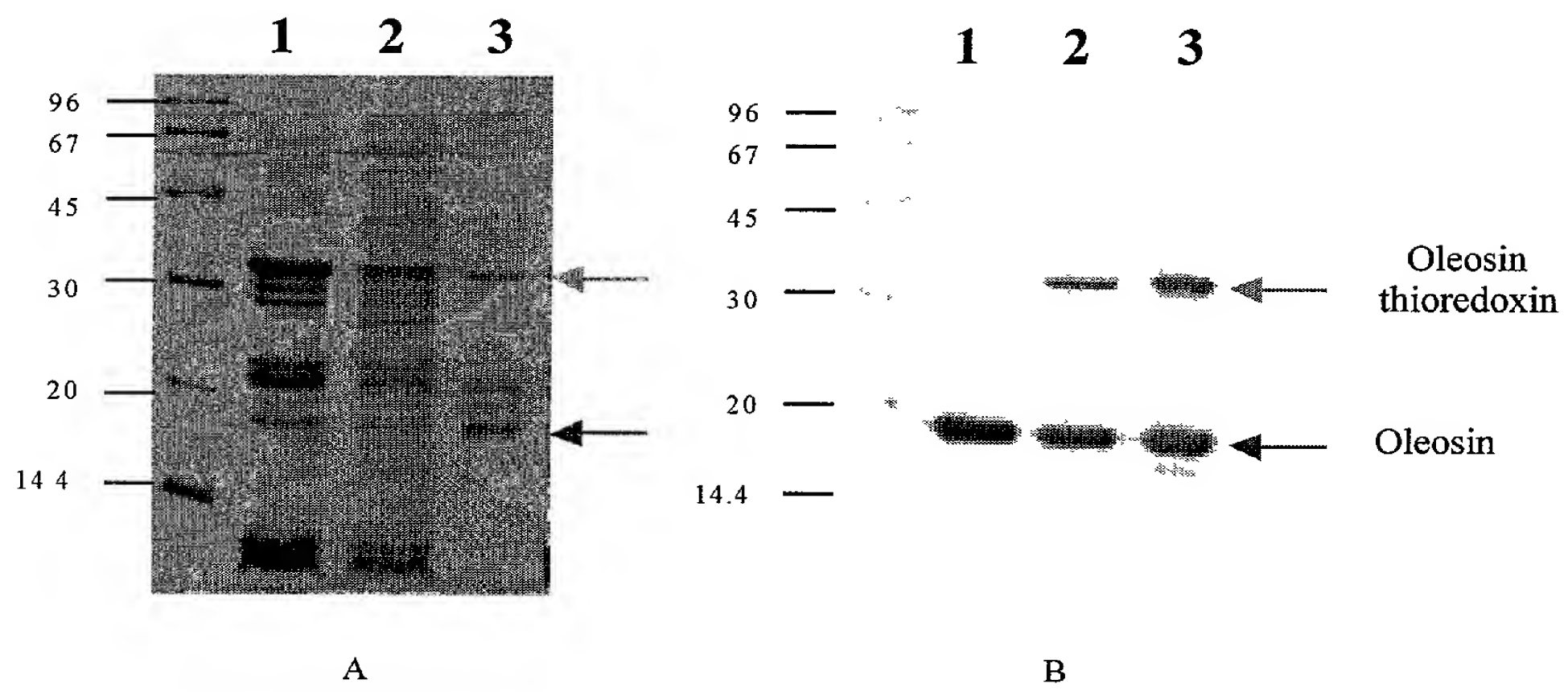
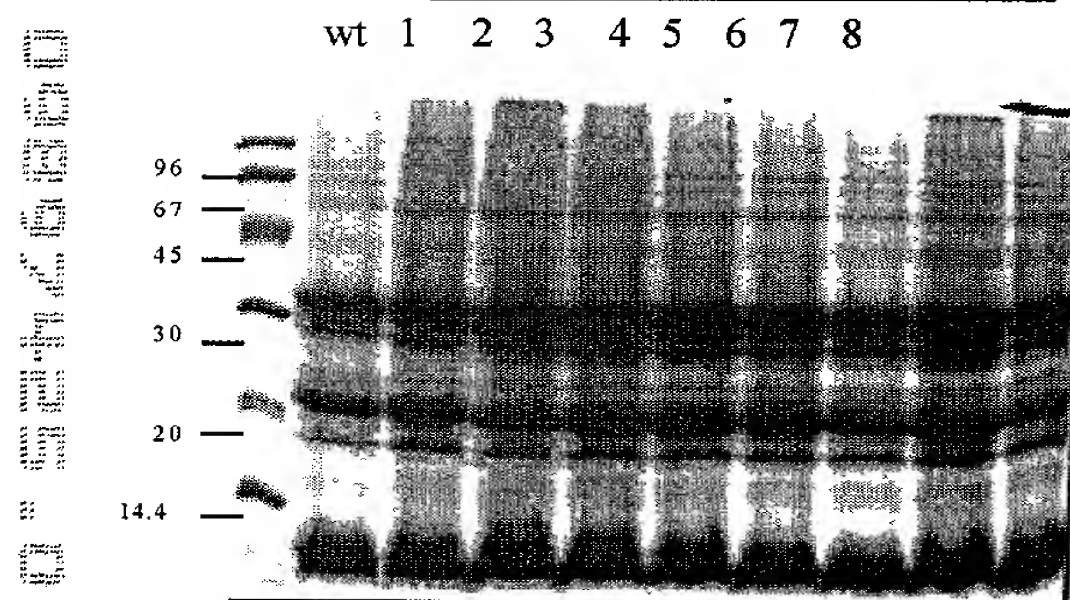


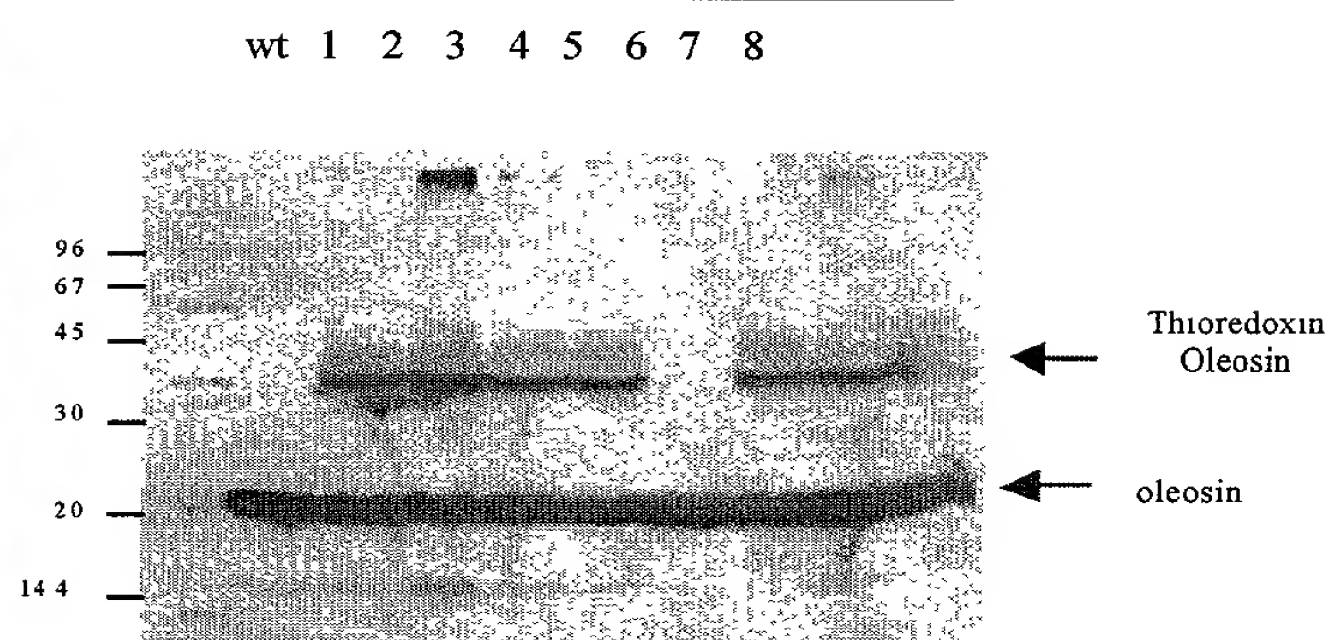
FIGURE 19

PSBS2521 transformants



A

PSBS2521 transformants



B

FIGURE 20

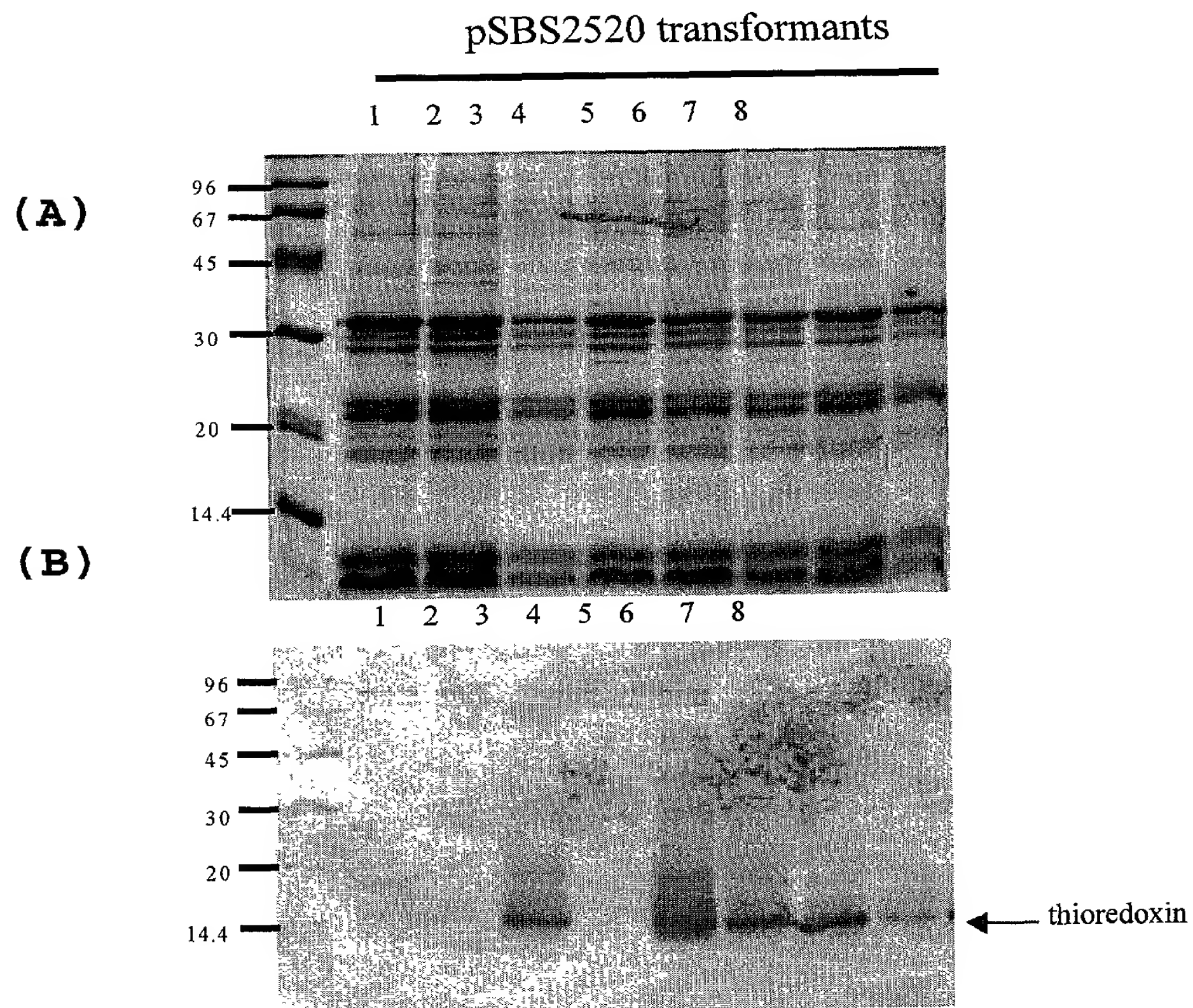


FIGURE 21

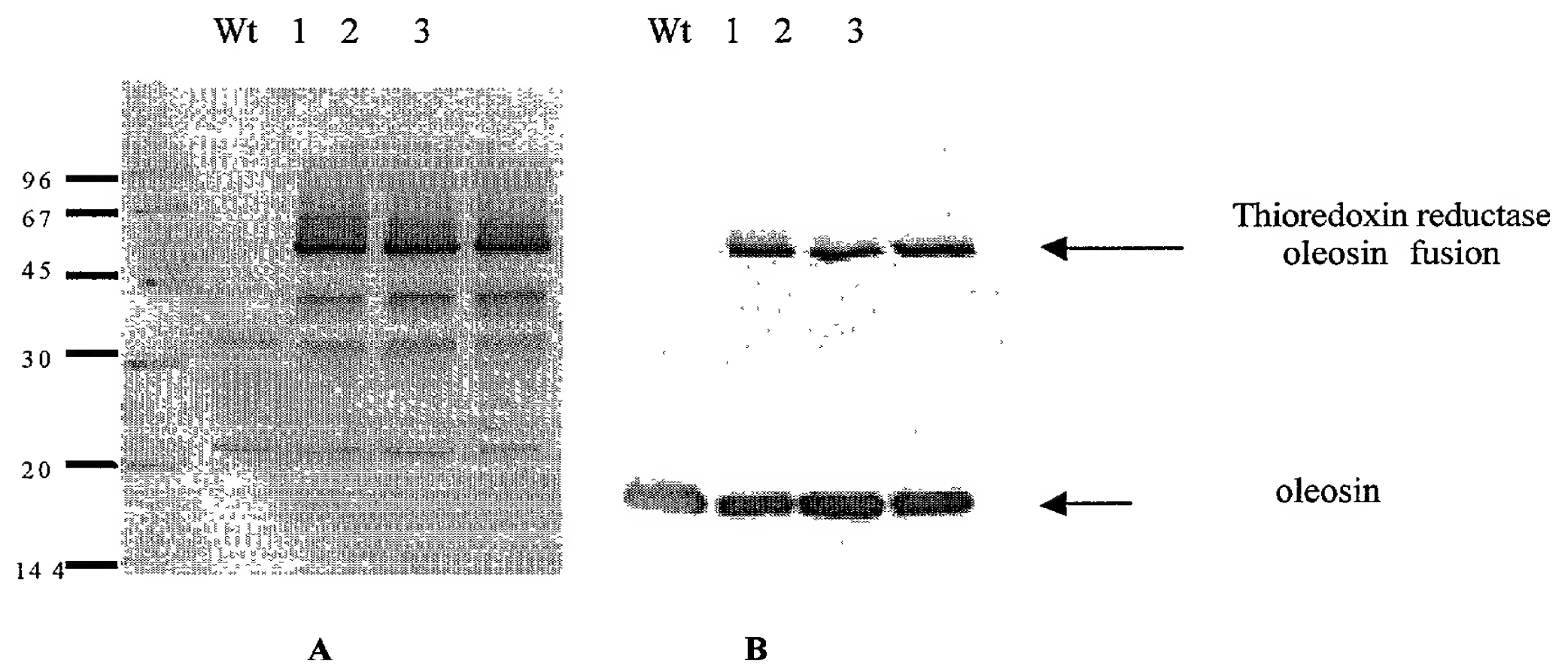


FIGURE 22

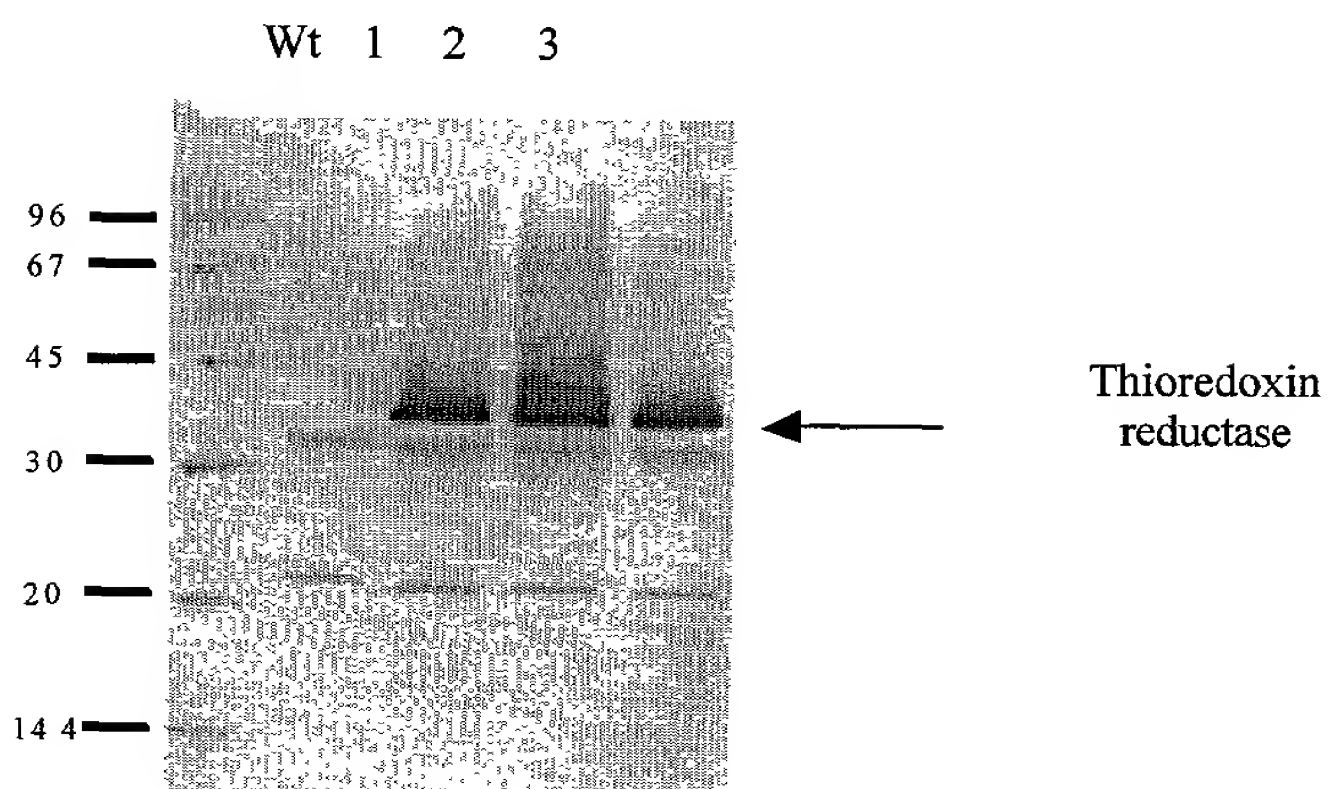


FIGURE 23

